



SEQUENCE LISTING

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Li, Liming
Ma, Jiyan
Liu, Jia-Jia
Sondheimer, Neal
Scheibel, Thomas

<120> RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS
AND METHODS COMPRISING SAME

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<141> 2000-06-09

<150> US 06/138,833

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Ser	Asn	Ile	Asn	Phe	Glu	Phe	Ser	Thr	Gly	Val	Asn	Asn	Asn	Asn	Asn
			35				40					45			
Asn	Asn	Ser	Ser	Ser	Asn	Asn	Asn	Asn	Val	Gln	Asn	Asn	Asn	Ser	Gly
			50				55				60				
Arg	Asn	Gly	Ser	Gln	Asn	Asn	Asp	Asn	Glu	Asn	Asn	Ile	Lys	Asn	Thr
					70					75					80
Leu	Glu	Gln	His	Arg	Gln	Gln	Gln	Gln	Ala	Phe	Ser	Asp	Met	Ser	His
				85					90					95	
Val	Glu	Tyr	Ser	Arg	Ile	Thr	Lys	Phe	Phe	Gln	Glu	Gln	Pro	Leu	Glu
			100					105						110	
Gly	Tyr	Thr	Leu	Phe	Ser	His	Arg	Ser	Ala	Pro	Asn	Gly	Phe	Lys	Val
			115				120					125			
Ala	Ile	Val	Leu	Ser	Glu	Leu	Gly	Phe	His	Tyr	Asn	Thr	Ile	Phe	Leu
			130				135				140				
Asp	Phe	Asn	Leu	Gly	Glu	His	Arg	Ala	Pro	Glu	Phe	Val	Ser	Val	Asn
			145			150				155					160
Pro	Asn	Ala	Arg	Val	Pro	Ala	Leu	Ile	Asp	His	Gly	Met	Asp	Asn	Leu
				165					170					175	
Ser	Ile	Trp	Glu	Ser	Gly	Ala	Ile	Leu	Leu	His	Leu	Val	Asn	Lys	Tyr
			180					185					190		
Tyr	Lys	Glu	Thr	Gly	Asn	Pro	Leu	Leu	Trp	Ser	Asp	Asp	Leu	Ala	Asp
			195				200					205			
Gln	Ser	Gln	Ile	Asn	Ala	Trp	Leu	Phe	Phe	Gln	Thr	Ser	Gly	His	Ala
			210				215				220				
Pro	Met	Ile	Gly	Gln	Ala	Leu	His	Phe	Arg	Tyr	Phe	His	Ser	Gln	Lys
					230					235					240
Ile	Ala	Ser	Ala	Val	Glu	Arg	Tyr	Thr	Asp	Glu	Val	Arg	Arg	Val	Tyr
				245					250					255	
Gly	Val	Val	Glu	Met	Ala	Leu	Ala	Glu	Arg	Arg	Glu	Ala	Leu	Val	Met
			260					265					270		
Glu	Leu	Asp	Thr	Glu	Asn	Ala	Ala	Ala	Tyr	Ser	Ala	Gly	Thr	Thr	Pro
			275				280					285			
Met	Ser	Gln	Ser	Arg	Phe	Phe	Asp	Tyr	Pro	Val	Trp	Leu	Val	Gly	Asp
			290				295				300				
Lys	Leu	Thr	Ile	Ala	Asp	Leu	Ala	Phe	Val	Pro	Trp	Asn	Asn	Val	Val

305	310	315	320
Asp Arg Ile Gly Ile Asn Ile Lys Ile Glu Phe Pro Glu Val Tyr Lys			
	325	330	335
Trp Thr Lys His Met Met Arg Arg Pro Ala Val Ile Lys Ala Leu Arg			
	340	345	350

Gly Glu

<210> 5
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FLAG peptide

<400> 5
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 6
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FLAG peptide

<400> 6
 Asp Tyr Lys Asp Glu Asp Asp Lys
 1 5

<210> 7
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Strep epitope

<400> 7
 Ala Trp Arg His Pro Gln Phe Gly Gly
 1 5

<210> 8
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hemagglutinin epitope

<400> 8
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ile Glu Gly Arg
 1 5 10

<210> 9
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: myc epitope

<400> 9
Glu Gln Lys Leu Leu Ser Glu Glu Asp Leu Asn
1 5 10

<210> 10
<211> 9
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 10
Pro Gln Gly Gly Tyr Gln Gln Tyr Asn
1 5

<210> 11
<211> 445
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CUP1 promoter

<400> 11
ccattaccga catttgggcg ctatacgtgc atatgttcat gtatgtatct gtatttaaaa 60
cacttttgta ttatttttcc tcatatatgt gtatagggtt atacggatga tttaattatt 120
acttcaccac cttttatttc aggtgatat cttagccttg ttactagtta gaaaaagaca 180
tttttgctgt cagtcactgt caagagattc ttttgctggc atttcttcta gaagcaaaaa 240
gagcgatgcy tcttttccgc tgaaccgttc cagcaaaaaa gactaccaac gcaatatgga 300
ttgtcagaat catataaaag agaagcaaat aactccttgc cttgtatcaa ttgcattata 360
atatcttctt gttagtgcaa tatcatatag aagtcacga aatagatatt aagaaaaaca 420
aactgtacaa tcaatcaatc aatca 445

<210> 12
<211> 717
<212> DNA
<213> *Aequorea victoria*

<400> 12
atgtctaaag gtgaagaatt attcactggg gttgtcccaa ttttggttga attagatggg 60
gatgttaatg gtcacaaatt ttctgtctcc ggtgaagggtg aaggatgatgc tacttacggg 120
aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180
gtcactactt tcgggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240

catgactttt tcaagtctgc catgccagaa gggtatgttc aagaaagaac tattttttttc 300
aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaagggtga taccttagtt 360
aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420
ttggaataca actataactc tcacaatggt tacatcatgg ctgacaaaca aaagaatggg 480
atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540
cattatcaac aaaataactcc aattgggtgat ggtccagtct tgttaccaga caaccattac 600
ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catggtcttg 660
ttagaatttg ttactgctgc tgggtattacc catggtatgg atgaattgta caaataa 717

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HA
tag-encoding sequence

<400> 13
taccatacg acgtcccaga ctacgct 27

<210> 14
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: yeast
Sup35Rdelta2-5 encoding sequence

<220>
<221> CDS
<222> (1)..(645)

<400> 14
atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac 48
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1 5 10 15
agc cag aac ggt aac caa caa caa ggt aac aac aga tac caa ggt tat 96
Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
20 25 30
caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat 144
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
35 40 45
tac caa ggt tat tct ggg tac cca caa ggt ggc cgt gga aat tac aaa 192
Tyr Gln Gly Tyr Ser Gly Tyr Pro Gln Gly Gly Arg Gly Asn Tyr Lys
50 55 60
aac ttc aac tac aat aac aat ttg caa gga tat caa gct ggt ttc caa 240
Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln
65 70 75 80

cca cag tct caa ggt atg tct ttg aac gac ttt caa aag caa caa aag	288
Pro Gln Ser Gln Gly Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys	
85 90 95	
cag gcc gct ccc aaa cca aag aag act ttg aag ctt gtc tcc agt tcc	336
Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser	
100 105 110	
ggt atc aag ttg gcc aat gct acc aag aag gtt ggc aca aaa cct gcc	384
Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala	
115 120 125	
gaa tct gat aag aaa gag gaa gag aag tct gct gaa acc aaa gaa cca	432
Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser Ala Glu Thr Lys Glu Pro	
130 135 140	
act aaa gag cca aca aag gtc gaa gaa cca gtt aaa aag gag gag aaa	480
Thr Lys Glu Pro Thr Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys	
145 150 155 160	
cca gtc cag act gaa gaa aag acg gag gaa aaa tcg gaa ctt cca aag	528
Pro Val Gln Thr Glu Glu Lys Thr Glu Glu Lys Ser Glu Leu Pro Lys	
165 170 175	
gta gaa gac ctt aaa atc tct gaa tca aca cat aat acc aac aat gcc	576
Val Glu Asp Leu Lys Ile Ser Glu Ser Thr His Asn Thr Asn Asn Ala	
180 185 190	
aat gtt acc agt gct gat gcc ttg atc aag gaa cag gaa gaa gaa gtg	624
Asn Val Thr Ser Ala Asp Ala Leu Ile Lys Glu Gln Glu Glu Val	
195 200 205	
gat gac gaa gtt gtt aac gat	645
Asp Asp Glu Val Val Asn Asp	
210 215	

<210> 15

<211> 215

<212> PRT

<213> Artificial Sequence

<400> 15

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
1 5 10 15

Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
20 25 30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
35 40 45

Tyr Gln Gly Tyr Ser Gly Tyr Pro Gln Gly Gly Arg Gly Asn Tyr Lys
50 55 60

Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln
65 70 75 80

Pro Gln Ser Gln Gly Met Ser Leu Asn Asp Phe Gln Lys Gln Gln Lys
85 90 95

Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser
100 105 110

Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys Val Gly Thr Lys Pro Ala
 115 120 125
 Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser Ala Glu Thr Lys Glu Pro
 130 135 140
 Thr Lys Glu Pro Thr Lys Val Glu Glu Pro Val Lys Lys Glu Glu Lys
 145 150 155 160
 Pro Val Gln Thr Glu Glu Lys Thr Glu Glu Lys Ser Glu Leu Pro Lys
 165 170 175
 Val Glu Asp Leu Lys Ile Ser Glu Ser Thr His Asn Thr Asn Asn Ala
 180 185 190
 Asn Val Thr Ser Ala Asp Ala Leu Ile Lys Glu Gln Glu Glu Val
 195 200 205
 Asp Asp Glu Val Val Asn Asp
 210 215

<210> 16

<211> 813

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: yeast
Sup35R2E2 encoding sequence

<220>

<221> CDS

<222> (1)..(813)

<400> 16

atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac	48
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr	
1 5 10 15	
agc cag aac ggt aac caa caa caa ggt aac aac aga tac caa ggt tat	96
Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr	
20 25 30	
caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat	144
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn	
35 40 45	
tac caa ggt tat tct ggg tac caa caa ggt ggc tat caa cag tac aat	192
Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn	
50 55 60	
ccc caa ggt ggc tat caa cag tac aat ccc caa ggt ggc tat caa cag	240
Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln	
65 70 75 80	
tac aat ccc gac gcc ggt tac cag caa cag tat aat cct caa gga ggc	288
Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly	
85 90 95	
tat caa cag tac aat cct caa ggc ggt tat cag cag caa ttc aat cca	336
Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro	
100 105 110	

caa ggt ggc cgt gga aat tac aaa aac ttc aac tac aat aac aat ttg	384
Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu	
115 120 125	
caa gga tat caa gct ggt ttc caa cca cag tct caa ggt atg tct ttg	432
Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu	
130 135 140	
aac gac ttt caa aag caa caa aag cag gcc gct ccc aaa cca aag aag	480
Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys	
145 150 155 160	
act ttg aag ctt gtc tcc agt tcc ggt atc aag ttg gcc aat gct acc	528
Thr Leu Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr	
165 170 175	
aag aag gtt ggc aca aaa cct gcc gaa tct gat aag aaa gag gaa gag	576
Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu	
180 185 190	
aag tct gct gaa acc aaa gaa cca act aaa gag cca aca aag gtc gaa	624
Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu	
195 200 205	
gaa cca gtt aaa aag gag gag aaa cca gtc cag act gaa gaa aag acg	672
Glu Pro Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr	
210 215 220	
gag gaa aaa tcg gaa ctt cca aag gta gaa gac ctt aaa atc tct gaa	720
Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu	
225 230 235 240	
tca aca cat aat acc aac aat gcc aat gtt acc agt gct gat gcc ttg	768
Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu	
245 250 255	
atc aag gaa cag gaa gaa gaa gtg gat gac gaa gtt gtt aac gat	813
Ile Lys Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp	
260 265 270	

<210> 17

<211> 271

<212> PRT

<213> Artificial Sequence

<400> 17

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr	
1 5 10 15	
Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr	
20 25 30	
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn	
35 40 45	
Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn	
50 55 60	
Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln	
65 70 75 80	
Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly	

85										90					95				
Tyr	Gln	Gln	Tyr	Asn	Pro	Gln	Gly	Gly	Tyr	Gln	Gln	Gln	Phe	Asn	Pro				
			100					105					110						
Gln	Gly	Gly	Arg	Gly	Asn	Tyr	Lys	Asn	Phe	Asn	Tyr	Asn	Asn	Asn	Leu				
		115					120					125							
Gln	Gly	Tyr	Gln	Ala	Gly	Phe	Gln	Pro	Gln	Ser	Gln	Gly	Met	Ser	Leu				
		130				135					140								
Asn	Asp	Phe	Gln	Lys	Gln	Gln	Lys	Gln	Ala	Ala	Pro	Lys	Pro	Lys	Lys				
				150					155						160				
Thr	Leu	Lys	Leu	Val	Ser	Ser	Ser	Gly	Ile	Lys	Leu	Ala	Asn	Ala	Thr				
				165				170					175						
Lys	Lys	Val	Gly	Thr	Lys	Pro	Ala	Glu	Ser	Asp	Lys	Lys	Glu	Glu	Glu				
			180					185					190						
Lys	Ser	Ala	Glu	Thr	Lys	Glu	Pro	Thr	Lys	Glu	Pro	Thr	Lys	Val	Glu				
		195					200					205							
Glu	Pro	Val	Lys	Lys	Glu	Glu	Lys	Pro	Val	Gln	Thr	Glu	Glu	Lys	Thr				
		210				215					220								
Glu	Glu	Lys	Ser	Glu	Leu	Pro	Lys	Val	Glu	Asp	Leu	Lys	Ile	Ser	Glu				
				230					235						240				
Ser	Thr	His	Asn	Thr	Asn	Asn	Ala	Asn	Val	Thr	Ser	Ala	Asp	Ala	Leu				
				245				250					255						
Ile	Lys	Glu	Gln	Glu	Glu	Glu	Val	Asp	Asp	Glu	Val	Val	Asn	Asp					
			260					265					270						

<210> 18
 <211> 641
 <212> DNA
 <213> MOUSE

<220>
 <221> CDS
 <222> (1)..(633)

<400> 18																
atg	tct	aaa	aag	cgg	cca	aag	cct	gga	ggg	tgg	aac	acc	ggt	gga	agc	48
Met	Ser	Lys	Lys	Arg	Pro	Lys	Pro	Gly	Gly	Trp	Asn	Thr	Gly	Gly	Ser	
1				5				10					15			
cgg	tat	ccc	ggg	cag	gga	agc	cct	gga	ggc	aac	cgt	tac	cca	cct	cag	96
Arg	Tyr	Pro	Gly	Gln	Gly	Ser	Pro	Gly	Gly	Asn	Arg	Tyr	Pro	Pro	Gln	
			20					25					30			
ggt	ggc	acc	tgg	ggg	cag	ccc	cac	ggt	ggt	ggc	tgg	gga	caa	ccc	cat	144
Gly	Gly	Thr	Trp	Gly	Gln	Pro	His	Gly	Gly	Gly	Trp	Gly	Gln	Pro	His	
			35				40					45				
ggg	ggc	agc	tgg	gga	caa	cct	cat	ggt	ggt	agt	tgg	ggt	cag	ccc	cat	192
Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	
		50				55					60					
ggc	ggt	gga	tgg	ggc	caa	gga	ggg	ggt	acc	cat	aat	cag	tgg	aac	aag	240

Gly 65	Gly	Gly	Trp	Gly	Gln 70	Gly	Gly	Gly	Thr	His 75	Asn	Gln	Trp	Asn	Lys 80	
ccc Pro	agc Ser	aaa Lys	cca Pro	aaa Lys 85	acc Thr	aac Asn	ctc Leu	aag Lys	cat His 90	gtg Val	gca Ala	ggg Gly	gct Ala	gcg Ala 95	gca Ala	288
gct Ala	ggg Gly	gca Ala	gta Val 100	gtg Val	ggg Gly	ggc Gly	ctt Leu 105	ggt Gly	ggc Gly	tac Tyr	atg Met	ctg Leu 110	ggg Gly	agc Ser	gcc Ala	336
gtg Val	agc Ser	agg Arg 115	ccc Pro	atg Met	atc Ile	cat His	ttt Phe 120	ggc Gly	aac Asn	gac Asp	tgg Trp	gag Glu 125	gac Asp	cgc Arg	tac Tyr	384
tac Tyr	cgt Arg 130	gaa Glu	aac Asn	atg Met	tac Tyr	cgc Arg 135	tac Tyr	cct Pro	aac Asn	caa Gln	gtg Val 140	tac Tyr	tac Tyr	agg Arg	cca Pro	432
gtg Val 145	gat Asp	cag Gln	tac Tyr	agc Ser	aac Asn 150	cag Gln	aac Asn	aac Asn	ttc Phe	gtg Val 155	cac His	gac Asp	tgc Cys	gtc Val	aat Asn 160	480
atc Ile	acc Thr	atc Ile	aag Lys 165	cag Gln	cac His	acg Thr	gtc Val	acc Thr	acc Thr	acc Thr	acc Thr	aag Lys	ggg Gly	gag Glu 175	aac Asn	528
ttc Phe	acc Thr	gag Glu	acc Thr 180	gat Asp	gtg Val	aag Lys	atg Met	atg Met	gag Glu	cgc Arg	gtg Val	gtg Val	gag Glu 190	cag Gln	atg Met	576
tgc Cys	gtc Val	acc Thr 195	cag Gln	tac Tyr	cag Gln	aag Lys	gag Glu 200	tcc Ser	cag Gln	gcc Ala	tat Tyr	tac Tyr 205	gac Asp	ggg Gly	aga Arg	624
aga Arg	tcc Ser	agc Ser 210	tgataacc													641

<210> 19
 <211> 211
 <212> PRT
 <213> MOUSE

Met 1	Ser	Lys	Lys	Arg 5	Pro	Lys	Pro	Gly	Gly	Trp	Asn	Thr	Gly	Gly	Ser 15
Arg	Tyr	Pro	Gly 20	Gln	Gly	Ser	Pro	Gly 25	Gly	Asn	Arg	Tyr	Pro 30	Pro	Gln
Gly	Gly	Thr 35	Trp	Gly	Gln	Pro	His 40	Gly	Gly	Gly	Trp	Gly 45	Gln	Pro	His
Gly	Gly	Ser 50	Trp	Gly	Gln	Pro	His 55	Gly	Gly	Ser	Trp 60	Gly	Gln	Pro	His
Gly 65	Gly	Gly	Trp	Gly	Gln	Gly	Gly	Gly	Thr	His 75	Asn	Gln	Trp	Asn	Lys 80
Pro	Ser	Lys	Pro	Lys 85	Thr	Asn	Leu	Lys	His 90	Val	Ala	Gly	Ala	Ala 95	Ala

Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser Ala
100 105 110

Val Ser Arg Pro Met Ile His Phe Gly Asn Asp Trp Glu Asp Arg Tyr
115 120 125

Tyr Arg Glu Asn Met Tyr Arg Tyr Pro Asn Gln Val Tyr Tyr Arg Pro
130 135 140

Val Asp Gln Tyr Ser Asn Gln Asn Asn Phe Val His Asp Cys Val Asn
145 150 155 160

Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu Asn
165 170 175

Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg Val Val Glu Gln Met
180 185 190

Cys Val Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly Arg
195 200 205

Arg Ser Ser
210

<210> 20
<211> 644
<212> DNA
<213> Mesocricetus auratus

<220>
<221> CDS
<222> (1)..(636)

<400> 20
atg tct aag aag cgg cca aag cct gga ggg tgg aac act ggc gga agc 48
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser
1 5 10 15

cga tac cct ggg cag ggc agc cct gga ggc aac cgt tac cca cct cag 96
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
20 25 30

ggt ggc ggc aca tgg ggg caa ccc cat ggt ggt ggc tgg gga cag ccc 144
Gly Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
35 40 45

cat ggt ggt ggc tgg gga cag ccc cat ggt ggt ggc tgg ggt cag ccc 192
His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
50 55 60

cat ggt ggt ggc tgg ggt caa gga ggt ggc acc cac aat cag tgg aac 240
His Gly Gly Gly Trp Gly Gln Gly Gly Thr His Asn Gln Trp Asn
65 70 75 80

aag ccc agt aag cca aaa acc aac atg aag cac atg gcc ggc gct gct 288
Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met Ala Gly Ala Ala
85 90 95

gcg gca ggg gcc gtg gtg ggg ggc ctt ggt ggc tac atg ctg ggg agt 336
Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser
100 105 110

gcc atg agc agg ccc atg atg cat ttt ggc aat gac tgg gag gac cgc	384
Ala Met Ser Arg Pro Met Met His Phe Gly Asn Asp Trp Glu Asp Arg	
115 120 125	
tac tac cgt gaa aac atg aac cgc tac cct aac caa gtg tat tac cgg	432
Tyr Tyr Arg Glu Asn Met Asn Arg Tyr Pro Asn Gln Val Tyr Tyr Arg	
130 135 140	
cca gtg gac cag tac aac aac cag aac aac ttt gtg cac gat tgt gtc	480
Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val	
145 150 155 160	
aac atc acc atc aag cag cac aca gtc acc acc acc acc aag ggg gag	528
Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu	
165 170 175	
aac ttc acg gag acc gac atc aag ata atg gag cgc gtg gtg gag cag	576
Asn Phe Thr Glu Thr Asp Ile Lys Ile Met Glu Arg Val Val Glu Gln	
180 185 190	
atg tgt acc acc cag tat cag aag gag tcc cag gcc tac tac gat gga	624
Met Cys Thr Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly	
195 200 205	
aga agg tcc agc tgataacc	644
Arg Arg Ser Ser	
210	

<210> 21
 <211> 212
 <212> PRT
 <213> Mesocricetus auratus

<400> 21	
Met Ser Lys Lys Arg Pro Lys Pro Gly Gly Trp Asn Thr Gly Gly Ser	
1 5 10 15	
Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln	
20 25 30	
Gly Gly Gly Thr Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro	
35 40 45	
His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro	
50 55 60	
His Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His Asn Gln Trp Asn	
65 70 75 80	
Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met Ala Gly Ala Ala	
85 90 95	
Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr Met Leu Gly Ser	
100 105 110	
Ala Met Ser Arg Pro Met Met His Phe Gly Asn Asp Trp Glu Asp Arg	
115 120 125	
Tyr Tyr Arg Glu Asn Met Asn Arg Tyr Pro Asn Gln Val Tyr Tyr Arg	
130 135 140	
Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val	

145 150 155 160
 Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys Gly Glu
 165 170 175
 Asn Phe Thr Glu Thr Asp Ile Lys Ile Met Glu Arg Val Val Glu Gln
 180 185 190
 Met Cys Thr Thr Gln Tyr Gln Lys Glu Ser Gln Ala Tyr Tyr Asp Gly
 195 200 205
 Arg Arg Ser Ser
 210

<210> 22
 <211> 780
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 22
 Met Lys Lys Lys Asp Asn Ser Asp Asp Lys Asp Asn Val Ala Ser Gly
 1 5 10 15
 Gly Tyr Lys Asn Ala Ala Asp Ala Gly Ser Asn Asn Ala Ser Lys Lys
 20 25 30
 Ser Ser Tyr Arg Asn Trp Lys Gly Gly Asn Tyr Gly Gly Tyr Ser Tyr
 35 40 45
 Asn Ser Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr
 50 55 60
 Asn Asn Tyr Asn Asn Tyr Asn Lys Tyr Asn Gly Gly Tyr Lys Ser Thr
 65 70 75 80
 Tyr Lys Ser Ala Val Thr Asn Ser Gly Thr Thr Ser Ala Ser Thr Thr
 85 90 95
 Ser Thr Ser Asn Lys Ser Asn Thr Ser Ser Lys Cys Ser Thr Asp Cys
 100 105 110
 Lys Asn Lys Gly Lys Gly Asn Ser Thr Gly Lys Trp Lys Val Asp Val
 115 120 125
 Ser Lys Lys Lys Asn Ser Val Arg Ser Ala Met Ser Asn Ala Ser Gly
 130 135 140
 Lys Ala Tyr Asn Val Ala Asp Cys Ser Asp Lys Asn Thr Val Lys Arg
 145 150 155 160
 Ala Ala His Ala Asp Ser Asn Cys Met Ala Thr Cys Val Thr Asp Tyr
 165 170 175
 Ser Ser Gly Ala Lys Trp Ala Lys Met Ala Ala Ser Val Val Asp Arg
 180 185 190
 Arg Asp Ser Ala Asn Asp Thr Lys Asp Ala Val Val Thr Asp Val Ala
 195 200 205
 Thr Asp Lys Ala Lys Gly Tyr Lys Thr Asp Tyr Val Ser Asp Asn Asp
 210 215 220

Ser Arg Tyr Lys Val Asp Thr Asp Ser Lys Val Ser Val Lys Ser Ser
 225 230 235 240
 Ser Val Thr Val Ala Val Thr Ser Ser Val Asn Arg Ser Asn Ser Ser
 245 250 255
 Ser Ser Arg Thr Val Val Val Asn Thr Arg Val Asn Asn Arg Asn Ser
 260 265 270
 Gly Lys Val Val Asp Thr Ala Ser Val Arg Ala Lys Ala Asn Val Lys
 275 280 285
 Asp Asp Ala Asp Lys Asn Lys Ser Gly Arg Thr Gly Arg Asp Asp His
 290 295 300
 Lys Asp Lys Ala Asp Asp Ser Cys Val Lys Tyr Met Asn Asp Thr Val
 305 310 315 320
 Lys Tyr Met Ser Lys Thr Val Asp Ser Asn Val Asn Asp Trp Lys Arg
 325 330 335
 Asp Thr Ala Val Gly Gly Ser Asp Ser Arg Val Lys Asp His Asn Arg
 340 345 350
 Ala Tyr Lys Arg Ala Asp Asp Gly Val Asn Thr Asp Ser Ala Tyr Gly
 355 360 365
 Ser Arg Met Asn Lys Thr Asn Arg Lys Gly His Arg Tyr Gly Cys Gly
 370 375 380
 Arg Asn Gly Ala Gly Lys Ser Thr Met Arg Ala Ala Asn Gly Asp Gly
 385 390 395 400
 Asp Lys Asp Thr Arg Thr Cys Val His Lys Gly Gly Asp Asp Val Ser
 405 410 415
 Ala Asp Ser Thr Ser Arg Ala Ala Ala Ser Val Gly Asp Arg Arg Ala
 420 425 430
 Thr Val Gly Ser Ser Gly Gly Trp Lys Met Lys Ala Arg Ala Met Lys
 435 440 445
 Ala Asp Asp Thr Asn His Asp Val Ser Asn Val Lys Trp Tyr His Thr
 450 455 460
 Asp Thr Ser Val Ser His Asp Ser Gly Asp Thr Val Cys Thr Asp His
 465 470 475 480
 Tyr Asn Lys Lys Ala Tyr Tyr Lys Gly Asn Ala Ala Val Lys Ala Lys
 485 490 495
 Ser Tyr Tyr Thr Thr Asp Ser Asn Ala Met Arg Gly Thr Gly Val Lys
 500 505 510
 Ser Asn Thr Arg Ala Val Ala Lys Met Thr Asp Val Thr Ser Tyr Gly
 515 520 525
 Ala Lys Ser Ser His Val Ser Cys Ser Ser Ser Ser Arg Val Ala Cys
 530 535 540
 Gly Asn Gly Ala Gly Lys Ser Thr Lys Thr Gly Val Asn Gly Lys Val
 545 550 555 560

Lys His Asn Arg Gly Tyr Ala His Ala His Val Asn His Lys Lys Thr
 565 570 575
 Ala Asn Tyr Trp Arg Tyr Gly Asp Asp Arg Val Lys Ser Arg Lys Ser
 580 585 590
 Asp Lys Met Met Thr Lys Asp Asp Asp Gly Arg Gly Lys Arg Ala Ala
 595 600 605
 Val Gly Arg Lys Lys Lys Ser Tyr Val Lys Trp Lys Tyr Trp Lys Lys
 610 615 620
 Tyr Asn Ser Trp Val Lys Asp Val Val His Gly Lys Val Lys Asp Asp
 625 630 635 640
 His Ala Ser Arg Gly Gly Tyr Arg Ser Val Thr Lys His Asp Val Gly
 645 650 655
 Asp Ser Ala Asn His Thr Gly Ser Ser Gly Gly Val Lys Val Val Ala
 660 665 670
 Gly Ala Met Trp Asn Asn His Val Asp Thr Asn Tyr Asp Arg Asp Ser
 675 680 685
 Gly Ala Ala Val Ala Arg Asp Trp Ser Gly Gly Val Val Met Ser His
 690 695 700
 Asn Asn Val Gly Ala Cys Trp Val Asn Gly Lys Met Val Lys Gly Ser
 705 710 715 720
 Ala Val Asp Ser Lys Asp Gly Gly Asn Ala Asp Ala Val Gly Lys Ala
 725 730 735
 Ser Asn Ala Lys Ser Val Asp Asp Asp Asp Ser Ala Asn Lys Val Lys
 740 745 750
 Arg Lys Lys Arg Thr Arg Asn Lys Lys Ala Arg Arg Arg Arg Tyr Trp
 755 760 765
 Ser Ser Lys Gly Thr Lys Val Asp Thr Asp Asp Asp
 770 775 780

<210> 23
 <211> 1075
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 23
 Met Asp Asn Lys Arg Leu Tyr Asn Gly Asn Leu Ser Asn Ile Pro Glu
 1 5 10 15
 Val Ile Asp Pro Gly Ile Thr Ile Pro Ile Tyr Glu Glu Asp Ile Arg
 20 25 30
 Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val Ser Asp
 35 40 45
 Lys Arg Gly Arg Ser Ser Ser Thr Ser Pro Gln Lys Ile Gly Ser Tyr
 50 55 60
 Arg Thr Arg Ala Gly Arg Phe Ser Asp Thr Leu Thr Asn Leu Leu Pro
 65 70 75 80

Ser	Ile	Ser	Ala	Lys	Leu	His	His	Ser	Lys	Lys	Ser	Thr	Pro	Val	Val	
				85					90					95		
Val	Val	Pro	Pro	Thr	Ser	Ser	Thr	Pro	Asp	Ser	Leu	Asn	Ser	Thr	Thr	
			100					105					110			
Tyr	Ala	Pro	Arg	Val	Ser	Ser	Asp	Ser	Phe	Thr	Val	Ala	Thr	Pro	Leu	
		115					120					125				
Ser	Leu	Gln	Ser	Thr	Thr	Thr	Arg	Thr	Arg	Thr	Arg	Asn	Asn	Thr	Val	
	130						135				140					
Ser	Ser	Gln	Ile	Thr	Ala	Ser	Ser	Ser	Leu	Thr	Thr	Asp	Val	Gly	Asn	
	145				150					155					160	
Ala	Thr	Ser	Ala	Asn	Ile	Trp	Ser	Ala	Asn	Ala	Glu	Ser	Asn	Thr	Ser	
				165					170					175		
Ser	Ser	Pro	Leu	Phe	Asp	Tyr	Pro	Leu	Ala	Thr	Ser	Tyr	Phe	Glu	Pro	
			180					185					190			
Leu	Thr	Arg	Phe	Lys	Ser	Thr	Asp	Asn	Tyr	Thr	Leu	Pro	Gln	Thr	Ala	
		195					200					205				
Gln	Leu	Asn	Ser	Phe	Leu	Glu	Lys	Asn	Gly	Asn	Pro	Asn	Ile	Trp	Ser	
	210					215					220					
Ser	Ala	Gly	Asn	Ser	Asn	Thr	Asp	His	Leu	Asn	Thr	Pro	Ile	Val	Asn	
	225				230					235					240	
Arg	Gln	Arg	Ser	Gln	Ser	Gln	Ser	Thr	Thr	Asn	Arg	Val	Tyr	Thr	Asp	
				245					250					255		
Ala	Pro	Tyr	Tyr	Gln	Gln	Pro	Ala	Gln	Asn	Tyr	Gln	Val	Gln	Val	Pro	
			260					265					270			
Pro	Arg	Val	Pro	Lys	Ser	Thr	Ser	Ile	Ser	Pro	Val	Ile	Leu	Asp	Asp	
		275					280					285				
Val	Asp	Pro	Ala	Ser	Ile	Asn	Trp	Ile	Thr	Ala	Asn	Gln	Lys	Val	Pro	
	290					295					300					
Leu	Val	Asn	Gln	Ile	Ser	Ala	Leu	Leu	Pro	Thr	Asn	Thr	Ile	Ser	Ile	
	305				310					315					320	
Ser	Asn	Val	Phe	Pro	Leu	Gln	Pro	Thr	Gln	Gln	His	Gln	Gln	Asn	Ala	
				325					330					335		
Val	Asn	Leu	Thr	Ser	Thr	Ser	Leu	Ala	Thr	Leu	Cys	Ser	Gln	Tyr	Gly	
			340					345					350			
Lys	Val	Leu	Ser	Ala	Arg	Thr	Leu	Arg	Gly	Leu	Asn	Met	Ala	Leu	Val	
		355					360					365				
Glu	Phe	Ser	Thr	Val	Glu	Ser	Ala	Ile	Cys	Ala	Leu	Glu	Ala	Leu	Gln	
	370					375					380					
Gly	Lys	Glu	Leu	Ser	Lys	Val	Gly	Ala	Pro	Ser	Thr	Val	Ser	Phe	Ala	
	385				390					395					400	
Arg	Val	Leu	Pro	Met	Tyr	Glu	Gln	Pro	Leu	Asn	Val	Asn	Gly	Phe	Asn	
				405					410					415		

Asn Thr Pro Lys Gln Pro Leu Leu Gln Glu Gln Leu Asn His Gly Val
 420 425 430
 Leu Asn Tyr Gln Leu Gln Gln Ser Leu Gln Gln Pro Glu Leu Gln Gln
 435 440 445
 Gln Pro Thr Ser Phe Asn Gln Pro Asn Leu Thr Tyr Cys Asn Pro Thr
 450 455 460
 Gln Asn Leu Ser His Leu Gln Leu Ser Ser Asn Glu Asn Glu Pro Tyr
 465 470 475 480
 Pro Phe Pro Leu Pro Pro Pro Ser Leu Ser Asp Ser Lys Lys Asp Ile
 485 490 495
 Leu His Thr Ile Ser Ser Phe Lys Leu Glu Tyr Asp His Leu Glu Leu
 500 505 510
 Asn His Leu Leu Gln Asn Ala Leu Lys Asn Lys Gly Val Ser Asp Thr
 515 520 525
 Asn Tyr Phe Gly Pro Leu Pro Glu His Asn Ser Lys Val Pro Lys Arg
 530 535 540
 Lys Asp Thr Phe Asp Ala Pro Lys Leu Arg Glu Leu Arg Lys Gln Phe
 545 550 555 560
 Asp Ser Asn Ser Leu Ser Thr Ile Glu Met Glu Gln Leu Ala Ile Val
 565 570 575
 Met Leu Asp Gln Leu Pro Glu Leu Ser Ser Asp Tyr Leu Gly Asn Thr
 580 585 590
 Val Ile Gln Lys Leu Phe Glu Asn Ser Ser Asn Ile Ile Arg Asp Ile
 595 600 605
 Met Leu Arg Lys Cys Asn Lys Tyr Leu Thr Ser Met Gly Val His Lys
 610 615 620
 Asn Gly Thr Trp Val Cys Gln Lys Ile Ile Lys Met Ala Asn Thr Pro
 625 630 635 640
 Arg Gln Ile Asn Leu Val Thr Ser Gly Val Ser Asp Tyr Cys Thr Pro
 645 650 655
 Leu Phe Asn Asp Gln Phe Gly Asn Tyr Val Ile Gln Gly Ile Leu Lys
 660 665 670
 Phe Gly Phe Pro Trp Asn Ser Phe Ile Phe Glu Ser Val Leu Ser His
 675 680 685
 Phe Trp Thr Ile Val Gln Asn Arg Tyr Gly Ser Arg Ala Val Arg Ala
 690 695 700
 Cys Leu Glu Ala Asp Ser Ile Ile Thr Gln Cys Gln Leu Leu Thr Ile
 705 710 715 720
 Thr Ser Leu Ile Ile Val Leu Ser Pro Tyr Leu Ala Thr Asp Thr Asn
 725 730 735
 Gly Thr Leu Leu Ile Thr Trp Leu Leu Asp Thr Cys Thr Leu Pro Asn
 740 745 750

Lys Asn Leu Ile Leu Cys Asp Lys Leu Val Asn Lys Asn Leu Val Lys
 755 760 765
 Leu Cys Cys His Lys Leu Gly Ser Leu Thr Val Leu Lys Ile Leu Asn
 770 775 780
 Leu Arg Gly Gly Glu Glu Glu Ala Leu Ser Lys Asn Lys Ile Ile His
 785 790 795 800
 Ala Ile Phe Asp Gly Pro Ile Ser Ser Asp Ser Ile Leu Phe Gln Ile
 805 810 815
 Leu Asp Glu Gly Asn Tyr Gly Pro Thr Phe Ile Tyr Lys Val Leu Thr
 820 825 830
 Ser Arg Ile Leu Asp Asn Ser Val Arg Asp Glu Ala Ile Thr Lys Ile
 835 840 845
 Arg Gln Leu Ile Leu Asn Ser Asn Ile Asn Leu Gln Ser Arg Gln Leu
 850 855 860
 Leu Glu Glu Val Gly Leu Ser Ser Ala Gly Ile Ser Pro Lys Gln Ser
 865 870 875 880
 Ser Lys Asn His Arg Lys Gln His Pro Gln Gly Phe His Ser Pro Gly
 885 890 895
 Arg Ala Arg Gly Val Ser Val Ser Ser Val Arg Ser Ser Asn Ser Arg
 900 905 910
 His Asn Ser Val Ile Gln Met Asn Asn Ala Gly Pro Thr Pro Ala Leu
 915 920 925
 Asn Phe Asn Pro Ala Pro Met Ser Glu Ile Asn Ser Tyr Phe Asn Asn
 930 935 940
 Gln Gln Val Val Tyr Ser Gly Asn Gln Asn Gln Asn Gln Asn Gly Asn
 945 950 955 960
 Ser Asn Gly Leu Asp Glu Leu Asn Ser Gln Phe Asp Ser Phe Arg Ile
 965 970 975
 Ala Asn Gly Thr Asn Leu Ser Leu Pro Ile Val Asn Leu Pro Asn Val
 980 985 990
 Ser Asn Asn Asn Asn Asn Tyr Asn Asn Ser Gly Tyr Ser Ser Gln Met
 995 1000 1005
 Asn Pro Leu Ser Arg Ser Val Ser His Asn Asn Asn Asn Asn Thr Asn
 1010 1015 1020
 Asn Tyr Asn Asn Asn Asp Asn Asp Asn Asn Asn Asn Asn Asn Asn Asn
 1025 1030 1035 1040
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
 1045 1050 1055
 Ser Asn Asn Asn Asn Asn Asn Asn Asp Thr Ser Leu Tyr Arg Tyr Arg Ser
 1060 1065 1070
 Tyr Gly Tyr
 1075

<210> 24
 <211> 76
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 24
 Met Ser Ala Asn Asp Tyr Tyr Gly Gly Thr Ala Gly Lys Ser Tyr Ser
 1 5 10 15
 Arg Ser Asn Ser Ser Ala His Asn Lys Thr Arg Gly Tyr Tyr Tyr His
 20 25 30
 Gly Tyr Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn
 35 40 45
 Gly Tyr Asn Gly Tyr Asn Gly His Val Tyr Val Arg Gly Asn Gly Cys
 50 55 60
 Ala Ala Cys Ala Ala Cys Cys Cys Thr Met Asp Met
 65 70 75

<210> 25
 <211> 380
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 25
 Met Ser Ser Asp Asp Asn Asp Tyr Gly Asp Asp Lys Thr Thr Thr Val
 1 5 10 15
 Lys Lys Asn Lys Ala Gly Ser Gly Thr Ser Asp Ala Ala Ala Ser Ser
 20 25 30
 Ser Asn Lys Asn Asn Asn Ser Asn Asn Ser Ser Ser Asn Asn Ser Asn
 35 40 45
 Asp Thr Ser Ser Ser Lys Asp Gly Thr Ala Asn Asp Lys Gly Ser Asn
 50 55 60
 Asp Thr Lys Asn Lys Lys Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn
 65 70 75 80
 Ala Ser Ser Ala Gly Ser Gly Trp Thr Met Ser Ser Ser Ser Val Thr
 85 90 95
 Thr Lys Arg Ser Lys Ala Asp Ser Lys Ser Cys Lys Met Gly Gly Asn
 100 105 110
 Trp Asp Thr Thr Asp Asn Arg Tyr Gly Lys Tyr Gly Thr Val Thr Asp
 115 120 125
 Lys Met Lys Asp Ala Thr Gly Arg Ser Arg Gly Gly Ser Lys Ser Ser
 130 135 140
 Val Asp Val Val Lys Thr His Asp Gly Lys Val Asp Lys Arg Ala Arg
 145 150 155 160
 Asp Asp Lys Thr Gly Lys Val Gly Gly Gly Asp Val Arg Lys Ser Trp
 165 170 175
 Gly Thr Asp Ala Met Asp Lys Asp Thr Gly Ser Arg Gly Gly Val Thr
 180 185 190

Tyr Asp Ser Ala Asp Ala Val Asp Arg Val Cys Asn Lys Asp Lys Asp
 195 200 205
 Arg Lys Lys Arg Ala Arg His Met Lys Ser Ser Asn Asn Gly Gly Asn
 210 215 220
 Asn Gly Gly Asn Asn Met Asn Arg Arg Gly Gly Asn Gly Asn Gly Asp
 225 230 235 240
 Asn Met Tyr Asn Met Met Gly Gly Tyr Asn Met Met Asn Ala Met Thr
 245 250 255
 Asp Tyr Tyr Lys Met Tyr Tyr Met Lys Thr Gly Met Asp Tyr Thr Met
 260 265 270
 Tyr Met Met Ala Met Met Met Gly Ala Met Asn Ala Met Thr Asn Asp
 275 280 285
 Ser Asn Ala Thr Gly Ser Ala Ser Asp Ser Asp Asn Asn Lys Ser Asn
 290 295 300
 Asp Val Thr Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Asn Asn Gly
 305 310 315 320
 Lys Gly Ser Tyr Asn Asp Asp His Asn Ser Gly Tyr Gly Tyr Asn Arg
 325 330 335
 Asp Arg Gly Asp Arg Asp Arg Asn Asp Arg Asp Arg Asp Tyr Asn His
 340 345 350
 Arg Ser Gly Gly Asn His Arg Arg Asn Gly Arg Gly Gly Arg Gly Gly
 355 360 365
 Tyr Asn Arg Arg Asn Asn Gly Tyr His Tyr Asn Arg
 370 375 380

<210> 26
 <211> 256
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 26
 Met Ser Ala Thr His Val Ser Val Val Asp Ala Val His Ala Asp Ala
 1 5 10 15
 Val Ser Ala Ser Ala Ala Asn Asp Val Ser Asn Ala Tyr Gly Ser His
 20 25 30
 Ser Val Asp Tyr Ala His His His Tyr Tyr Gly His Met His Gly Arg
 35 40 45
 Met His His Arg Gly Ser Asn Thr Arg Val Arg Asp Val Ser Asn Gly
 50 55 60
 Gly Met Lys Val Lys Asn Gly Ala Val Ala Ser Ala Ala Lys Ala Val
 65 70 75 80
 His Gly Lys Ser Ala Asn Val Val Tyr Ser Lys Ala Lys Arg Tyr Arg
 85 90 95
 Thr Met Lys Asn Gly Cys Ser Trp Asp Lys Asp Ala Arg Asn Ser Thr
 100 105 110

Thr Ser Ser Val Asn Thr Arg Asp Asp Gly Thr Gly Ala Ser Val Ala
 115 120 125
 Arg Asn Asn Arg Gly Ser Val Thr Val Arg Asp Asp Asn Arg Arg Ser
 130 135 140
 Asn Arg Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg
 145 150 155 160
 Gly Gly Ser Arg Gly Gly Gly Gly Arg Gly Gly Gly Arg Gly Gly
 165 170 175
 Tyr Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Tyr Ser Arg Gly Gly
 180 185 190
 Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Ser Arg Gly Gly Tyr Asp Ser
 195 200 205
 Arg Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Arg Asn Asp Tyr Gly
 210 215 220
 Arg Gly Ser Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Gly Arg Gly Asp
 225 230 235 240
 Tyr Gly Arg Asp Ala Tyr Arg Thr Arg Asp Ala Arg Arg Ser Thr Arg
 245 250 255

<210> 27
 <211> 286
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 27
 Met Ser Asp Ile Glu Glu Gly Thr Pro Thr Asn Asn Gly Gln Gln Lys
 1 5 10 15
 Glu Arg Arg Lys Ile Glu Ile Lys Phe Ile Glu Asn Lys Thr Arg Arg
 20 25 30
 His Val Thr Phe Ser Lys Arg Lys His Gly Ile Met Lys Lys Ala Phe
 35 40 45
 Glu Leu Ser Val Leu Thr Gly Thr Gln Val Leu Leu Leu Val Val Ser
 50 55 60
 Glu Thr Gly Leu Val Tyr Thr Phe Ser Thr Pro Lys Phe Glu Pro Ile
 65 70 75 80
 Val Thr Gln Gln Glu Gly Arg Asn Leu Ile Gln Ala Cys Leu Asn Ala
 85 90 95
 Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Asp Gly Asp Asp Asp Asp
 100 105 110
 Asp Asp Asp Asp Asp Gly Asn Asp Met Gln Arg Gln Gln Pro Gln Gln
 115 120 125
 Gln Gln Pro Gln Gln Gln Gln Val Leu Asn Ala His Ala Asn Ser
 130 135 140

Leu Gly His Leu Asn Gln Asp Gln Val Pro Ala Gly Ala Leu Lys Gln
 145 150 155 160
 Glu Val Lys Ser Gln Leu Leu Gly Gly Ala Asn Pro Asn Gln Asn Ser
 165 170 175
 Met Ile Gln Gln Gln Gln His His Thr Gln Asn Ser Gln Pro Gln Gln
 180 185 190
 Gln Gln Gln Gln Gln Pro Gln Gln Gln Met Ser Gln Gln Gln Met Ser
 195 200 205
 Gln His Pro Arg Pro Gln Gln Gly Ile Pro His Pro Gln Gln Ser Gln
 210 215 220
 Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln
 225 230 235 240
 Gln Gln Gln Gln Gln Pro Leu Thr Gly Ile His Gln Pro His Gln Gln
 245 250 255
 Ala Phe Ala Asn Ala Ala Ser Pro Tyr Leu Asn Ala Glu Gln Asn Ala
 260 265 270
 Ala Tyr Gln Gln Tyr Phe Gln Glu Pro Gln Gln Gly Gln Tyr
 275 280 285

<210> 28
 <211> 414
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 28
 Met Ala Lys Thr Thr Lys Val Lys Gly Asn Lys Lys Glu Val Lys Ala
 1 5 10 15
 Ser Lys Gln Ala Lys Glu Glu Lys Ala Lys Ala Val Ser Ser Ser Ser
 20 25 30
 Ser Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Glu Ser Glu
 35 40 45
 Ser Glu Ser Glu Ser Glu Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser
 50 55 60
 Glu Ser Ser Ser Ser Ser Ser Ser Asp Ser Glu Ser Glu Ala Glu Thr
 65 70 75 80
 Lys Lys Glu Glu Ser Lys Asp Ser Ser Ser Ser Ser Ser Asp Ser Ser
 85 90 95
 Ser Asp Glu Glu Glu Glu Glu Glu Lys Glu Glu Thr Lys Lys Glu Glu
 100 105 110
 Ser Lys Glu Ser Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Ser Asp
 115 120 125
 Ser Glu Ser Glu Lys Glu Glu Ser Asn Asp Lys Lys Arg Lys Ser Glu
 130 135 140
 Asp Ala Glu Glu Glu Glu Asp Glu Glu Ser Ser Asn Lys Lys Gln Lys
 145 150 155 160

Asn Glu Glu Thr Glu Glu Pro Ala Thr Ile Phe Val Gly Arg Leu Ser
 165 170 175
 Trp Ser Ile Asp Asp Glu Trp Leu Lys Lys Glu Phe Glu His Ile Gly
 180 185 190
 Gly Val Ile Gly Ala Arg Val Ile Tyr Glu Arg Gly Thr Asp Arg Ser
 195 200 205
 Arg Gly Tyr Gly Tyr Val Asp Phe Glu Asn Lys Ser Tyr Ala Glu Lys
 210 215 220
 Ala Ile Gln Glu Met Gln Gly Lys Glu Ile Asp Gly Arg Pro Ile Asn
 225 230 235 240
 Cys Asp Met Ser Thr Ser Lys Pro Ala Gly Asn Asn Asp Arg Ala Lys
 245 250 255
 Lys Phe Gly Asp Thr Pro Ser Glu Pro Ser Asp Thr Leu Phe Leu Gly
 260 265 270
 Asn Leu Ser Phe Asn Ala Asp Arg Asp Ala Ile Phe Glu Leu Phe Ala
 275 280 285
 Lys His Gly Glu Val Val Ser Val Arg Ile Pro Thr His Pro Glu Thr
 290 295 300
 Glu Gln Pro Lys Gly Phe Gly Tyr Val Gln Phe Ser Asn Met Glu Asp
 305 310 315 320
 Ala Lys Lys Ala Leu Asp Ala Leu Gln Gly Glu Tyr Ile Asp Asn Arg
 325 330 335
 Pro Val Arg Leu Asp Phe Ser Ser Pro Arg Pro Asn Asn Asp Gly Gly
 340 345 350
 Arg Gly Gly Ser Arg Gly Phe Gly Gly Arg Gly Gly Arg Gly Gly
 355 360 365
 Asn Arg Gly Phe Gly Gly Arg Gly Gly Ala Arg Gly Gly Arg Gly Gly
 370 375 380
 Phe Arg Pro Ser Gly Ser Gly Ala Asn Thr Ala Pro Leu Gly Arg Ser
 385 390 395 400
 Arg Asn Thr Ala Ser Phe Ala Gly Ser Lys Lys Thr Phe Asp
 405 410

<210> 29

<211> 405

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 29

Met Asp Thr Asp Lys Leu Ile Ser Glu Ala Glu Ser His Phe Ser Gln
 1 5 10 15
 Gly Asn His Ala Glu Ala Val Ala Lys Leu Thr Ser Ala Ala Gln Ser
 20 25 30
 Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
 35 40 45

Ile Ala Gly Tyr Val Met Asp Asn Arg Ser Gly Gly Ser Asp Ala Ser
 50 55 60
 Gln Asp Arg Ala Ala Gly Gly Gly Ser Ser Phe Met Asn Thr Leu Met
 65 70 75 80
 Ala Asp Ser Lys Gly Ser Ser Gln Thr Gln Leu Gly Lys Leu Ala Leu
 85 90 95
 Leu Ala Thr Val Met Thr His Ser Ser Asn Lys Gly Ser Ser Asn Arg
 100 105 110
 Gly Phe Asp Val Gly Thr Val Met Ser Met Leu Ser Gly Ser Gly Gly
 115 120 125
 Gly Ser Gln Ser Met Gly Ala Ser Gly Leu Ala Ala Leu Ala Ser Gln
 130 135 140
 Phe Phe Lys Ser Gly Asn Asn Ser Gln Gly Gln Gly Gln Gly Gln Gly
 145 150 155 160
 Gln Gly Gln Gly Gln Gly Gln Gly Gln Gly Ser Phe Thr Ala
 165 170 175
 Leu Ala Ser Leu Ala Ser Ser Phe Met Asn Ser Asn Asn Asn Asn Gln
 180 185 190
 Gln Gly Gln Asn Gln Ser Ser Gly Gly Ser Ser Phe Gly Ala Leu Ala
 195 200 205
 Ser Met Ala Ser Ser Phe Met His Ser Asn Asn Asn Gln Asn Ser Asn
 210 215 220
 Asn Ser Gln Gln Gly Tyr Asn Gln Ser Tyr Gln Asn Gly Asn Gln Asn
 225 230 235 240
 Ser Gln Gly Tyr Asn Asn Gln Gln Tyr Gln Gly Gly Asn Gly Gly Tyr
 245 250 255
 Gln Gln Gln Gln Gly Gln Ser Gly Gly Ala Phe Ser Ser Leu Ala Ser
 260 265 270
 Met Ala Gln Ser Tyr Leu Gly Gly Gly Gln Thr Gln Ser Asn Gln Gln
 275 280 285
 Gln Tyr Asn Gln Gln Gly Gln Asn Asn Gln Gln Gln Tyr Gln Gln Gln
 290 295 300
 Gly Gln Asn Tyr Gln His Gln Gln Gln Gly Gln Gln Gln Gln Gln Gly
 305 310 315 320
 His Ser Ser Ser Phe Ser Ala Leu Ala Ser Met Ala Ser Ser Tyr Leu
 325 330 335
 Gly Asn Asn Ser Asn Ser Asn Ser Ser Tyr Gly Gly Gln Gln Gln Ala
 340 345 350
 Asn Glu Tyr Gly Arg Pro Gln His Asn Gly Gln Gln Gln Ser Asn Glu
 355 360 365
 Tyr Gly Arg Pro Gln Tyr Gly Gly Asn Gln Asn Ser Asn Gly Gln His
 370 375 380

Glu Ser Phe Asn Phe Ser Gly Asn Phe Ser Gln Gln Asn Asn Asn Gly
 385 390 395 400

Asn Gln Asn Arg Tyr
 405

<210> 30

<211> 964

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 30

Met Pro Glu Gln Ala Gln Gln Gly Glu Gln Ser Val Lys Arg Arg Arg
 1 5 10 15

Val Thr Arg Ala Cys Asp Glu Cys Arg Lys Lys Lys Val Lys Cys Asp
 20 25 30

Gly Gln Gln Pro Cys Ile His Cys Thr Val Tyr Ser Tyr Glu Cys Thr
 35 40 45

Tyr Lys Lys Pro Thr Lys Arg Thr Gln Asn Ser Gly Asn Ser Gly Val
 50 55 60

Leu Thr Leu Gly Asn Val Thr Thr Gly Pro Ser Ser Ser Thr Val Val
 65 70 75 80

Ala Ala Ala Ala Ser Asn Pro Asn Lys Leu Leu Ser Asn Ile Lys Thr
 85 90 95

Glu Arg Ala Ile Leu Pro Gly Ala Ser Thr Ile Pro Ala Ser Asn Asn
 100 105 110

Pro Ser Lys Pro Arg Lys Tyr Lys Thr Lys Ser Thr Arg Leu Gln Ser
 115 120 125

Lys Ile Asp Arg Tyr Lys Gln Ile Phe Asp Glu Val Phe Pro Gln Leu
 130 135 140

Pro Asp Ile Asp Asn Leu Asp Ile Pro Val Phe Leu Gln Ile Phe His
 145 150 155 160

Asn Phe Lys Arg Asp Ser Gln Ser Phe Leu Asp Asp Thr Val Lys Glu
 165 170 175

Tyr Thr Leu Ile Val Asn Asp Ser Ser Ser Pro Ile Gln Pro Val Leu
 180 185 190

Ser Ser Asn Ser Lys Asn Ser Thr Pro Asp Glu Phe Leu Pro Asn Met
 195 200 205

Lys Ser Asp Ser Asn Ser Ala Ser Ser Asn Arg Glu Gln Asp Ser Val
 210 215 220

Asp Thr Tyr Ser Asn Ile Pro Val Gly Arg Glu Ile Lys Ile Ile Leu
 225 230 235 240

Pro Pro Lys Ala Ile Ala Leu Gln Phe Val Lys Ser Thr Trp Glu His
 245 250 255

Cys Cys Val Leu Leu Arg Phe Tyr His Arg Pro Ser Phe Ile Arg Gln
 260 265 270

Leu Asp Glu Leu Tyr Glu Thr Asp Pro Asn Asn Tyr Thr Ser Lys Gln
 275 280 285
 Met Gln Phe Leu Pro Leu Cys Tyr Ala Ala Ile Ala Val Gly Ala Leu
 290 295 300
 Phe Ser Lys Ser Ile Val Ser Asn Asp Ser Ser Arg Glu Lys Phe Leu
 305 310 315 320
 Gln Asp Glu Gly Tyr Lys Tyr Phe Ile Ala Ala Arg Lys Leu Ile Asp
 325 330 335
 Ile Thr Asn Ala Arg Asp Leu Asn Ser Ile Gln Ala Ile Leu Met Leu
 340 345 350
 Ile Ile Phe Leu Gln Cys Ser Ala Arg Leu Ser Thr Cys Tyr Thr Tyr
 355 360 365
 Ile Gly Val Ala Met Arg Ser Ala Leu Arg Ala Gly Phe His Arg Lys
 370 375 380
 Leu Ser Pro Asn Ser Gly Phe Ser Pro Ile Glu Ile Glu Met Arg Lys
 385 390 395 400
 Arg Leu Phe Tyr Thr Ile Tyr Lys Leu Asp Val Tyr Ile Asn Ala Met
 405 410 415
 Leu Gly Leu Pro Arg Ser Ile Ser Pro Asp Asp Phe Asp Gln Thr Leu
 420 425 430
 Pro Leu Asp Leu Ser Asp Glu Asn Ile Thr Glu Val Ala Tyr Leu Pro
 435 440 445
 Glu Asn Gln His Ser Val Leu Ser Ser Thr Gly Ile Ser Asn Glu His
 450 455 460
 Thr Lys Leu Phe Leu Ile Leu Asn Glu Ile Ile Ser Glu Leu Tyr Pro
 465 470 475 480
 Ile Lys Lys Thr Ser Asn Ile Ile Ser His Glu Thr Val Thr Ser Leu
 485 490 495
 Glu Leu Lys Leu Arg Asn Trp Leu Asp Ser Leu Pro Lys Glu Leu Ile
 500 505 510
 Pro Asn Ala Glu Asn Ile Asp Pro Glu Tyr Glu Arg Ala Asn Arg Leu
 515 520 525
 Leu His Leu Ser Phe Leu His Val Gln Ile Ile Leu Tyr Arg Pro Phe
 530 535 540
 Ile His Tyr Leu Ser Arg Asn Met Asn Ala Glu Asn Val Asp Pro Leu
 545 550 555 560
 Cys Tyr Arg Arg Ala Arg Asn Ser Ile Ala Val Ala Arg Thr Val Ile
 565 570 575
 Lys Leu Ala Lys Glu Met Val Ser Asn Asn Leu Leu Thr Gly Ser Tyr
 580 585 590
 Trp Tyr Ala Cys Tyr Thr Ile Phe Tyr Ser Val Ala Gly Leu Leu Phe
 595 600 605

Tyr Ile His Glu Ala Gln Leu Pro Asp Lys Asp Ser Ala Arg Glu Tyr
 610 615 620
 Tyr Asp Ile Leu Lys Asp Ala Glu Thr Gly Arg Ser Val Leu Ile Gln
 625 630 635 640
 Leu Lys Asp Ser Ser Met Ala Ala Ser Arg Thr Tyr Asn Leu Leu Asn
 645 650 655
 Gln Ile Phe Glu Lys Leu Asn Ser Lys Thr Ile Gln Leu Thr Ala Leu
 660 665 670
 His Ser Ser Pro Ser Asn Glu Ser Ala Phe Leu Val Thr Asn Asn Ser
 675 680 685
 Ser Ala Leu Lys Pro His Leu Gly Asp Ser Leu Gln Pro Pro Val Phe
 690 695 700
 Phe Ser Ser Gln Asp Thr Lys Asn Ser Phe Ser Leu Ala Lys Ser Glu
 705 710 715 720
 Glu Ser Thr Asn Asp Tyr Ala Met Ala Asn Tyr Leu Asn Asn Thr Pro
 725 730 735
 Ile Ser Glu Asn Pro Leu Asn Glu Ala Gln Gln Gln Asp Gln Val Ser
 740 745 750
 Gln Gly Thr Thr Asn Met Ser Asn Glu Arg Asp Pro Asn Asn Phe Leu
 755 760 765
 Ser Ile Asp Ile Arg Leu Asp Asn Asn Gly Gln Ser Asn Ile Leu Asp
 770 775 780
 Ala Thr Asp Asp Val Phe Ile Arg Asn Asp Gly Asp Ile Pro Thr Asn
 785 790 795 800
 Ser Ala Phe Asp Phe Ser Ser Ser Lys Ser Asn Ala Ser Asn Asn Ser
 805 810 815
 Asn Pro Asp Thr Ile Asn Asn Asn Tyr Asn Asn Val Ser Gly Lys Asn
 820 825 830
 Asn Asn Asn Asn Asn Ile Thr Asn Asn Ser Asn Asn Asn His Asn Asn
 835 840 845
 Asn Asn Asn Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 850 855 860
 Asn Asn Asn Asn Asn Ser Gly Asn Ser Ser Asn Asn Asn Asn Asn Asn
 865 870 875 880
 Asn Asn Asn Lys Asn Asn Asn Asp Phe Gly Ile Lys Ile Asp Asn Asn
 885 890 895
 Ser Pro Ser Tyr Glu Gly Phe Pro Gln Leu Gln Ile Pro Leu Ser Gln
 900 905 910
 Asp Asn Leu Asn Ile Glu Asp Lys Glu Glu Met Ser Pro Asn Ile Glu
 915 920 925
 Ile Lys Asn Glu Gln Asn Met Thr Asp Ser Asn Asp Ile Leu Gly Val
 930 935 940

Phe Asp Gln Leu Asp Ala Gln Leu Phe Gly Lys Tyr Leu Pro Leu Asn
 945 950 955 960

Tyr Pro Ser Glu

<210> 31

<211> 758

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 31

Met Asp Asn Thr Thr Asn Ile Asn Thr Asn Glu Arg Ser Ser Asn Thr
 1 5 10 15

Asp Phe Ser Ser Ala Pro Asn Ile Lys Gly Leu Asn Ser His Thr Gln
 20 25 30

Leu Gln Phe Asp Ala Asp Ser Arg Val Phe Val Ser Asp Val Met Ala
 35 40 45

Lys Asn Ser Lys Gln Leu Leu Tyr Ala His Ile Tyr Asn Tyr Leu Ile
 50 55 60

Lys Asn Asn Tyr Trp Asn Ser Ala Ala Lys Phe Leu Ser Glu Ala Asp
 65 70 75 80

Leu Pro Leu Ser Arg Ile Asn Gly Ser Ala Ser Gly Gly Lys Thr Ser
 85 90 95

Leu Asn Ala Ser Leu Lys Gln Gly Leu Met Asp Ile Ala Ser Lys Gly
 100 105 110

Asp Ile Val Ser Glu Asp Gly Leu Leu Pro Ser Lys Met Leu Met Asp
 115 120 125

Ala Asn Asp Thr Phe Leu Leu Glu Trp Trp Glu Ile Phe Gln Ser Leu
 130 135 140

Phe Asn Gly Asp Leu Glu Ser Gly Tyr Gln Gln Asp His Asn Pro Leu
 145 150 155 160

Arg Glu Arg Ile Ile Pro Ile Leu Pro Ala Asn Ser Lys Ser Asn Met
 165 170 175

Pro Ser His Phe Ser Asn Leu Pro Pro Asn Val Ile Pro Pro Thr Gln
 180 185 190

Asn Ser Phe Pro Val Ser Glu Glu Ser Phe Arg Pro Asn Gly Asp Gly
 195 200 205

Ser Asn Phe Asn Leu Asn Asp Pro Thr Asn Arg Asn Val Ser Glu Arg
 210 215 220

Phe Leu Ser Arg Thr Ser Gly Val Tyr Asp Lys Gln Asn Ser Ala Asn
 225 230 235 240

Phe Ala Pro Asp Thr Ala Ile Asn Ser Asp Ile Ala Gly Gln Gln Tyr
 245 250 255

Ala Thr Ile Asn Leu His Lys His Phe Asn Asp Leu Gln Ser Pro Ala
 260 265 270

Gln Pro Gln Gln Ser Ser Gln Gln Gln Ile Gln Gln Pro Gln His Gln
 275 280 285
 Pro Gln His Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 290 295 300
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 305 310 315 320
 Gln Gln Gln His Gln Gln Gln Gln Gln Thr Pro Tyr Pro Ile Val Asn
 325 330 335
 Pro Gln Met Val Pro His Ile Pro Ser Glu Asn Ser His Ser Thr Gly
 340 345 350
 Leu Met Pro Ser Val Pro Pro Thr Asn Gln Gln Phe Asn Ala Gln Thr
 355 360 365
 Gln Ser Ser Met Phe Ser Asp Gln Gln Arg Phe Phe Gln Tyr Gln Leu
 370 375 380
 His His Gln Asn Gln Gly Gln Ala Pro Ser Phe Gln Gln Ser Gln Ser
 385 390 395 400
 Gly Arg Phe Asp Asp Met Asn Ala Met Lys Met Phe Phe Gln Gln Gln
 405 410 415
 Ala Leu Gln Gln Asn Ser Leu Gln Gln Asn Leu Gly Asn Gln Asn Tyr
 420 425 430
 Gln Ser Asn Thr Arg Asn Asn Thr Ala Glu Glu Thr Thr Pro Thr Asn
 435 440 445
 Asp Asn Asn Ala Asn Gly Asn Ser Leu Leu Gln Glu His Ile Arg Ala
 450 455 460
 Arg Phe Asn Lys Met Lys Thr Ile Pro Gln Gln Met Lys Asn Gln Ser
 465 470 475 480
 Thr Val Ala Asn Pro Val Val Ser Asp Ile Thr Ser Gln Gln Gln Tyr
 485 490 495
 Met His Met Met Met Gln Arg Met Ala Ala Asn Gln Gln Leu Gln Asn
 500 505 510
 Ser Ala Phe Pro Pro Asp Thr Asn Arg Ile Ala Pro Ala Asn Asn Thr
 515 520 525
 Met Pro Leu Gln Pro Gly Asn Met Gly Ser Pro Val Ile Glu Asn Pro
 530 535 540
 Gly Met Arg Gln Thr Asn Pro Ser Gly Gln Asn Pro Met Ile Asn Met
 545 550 555 560
 Gln Pro Leu Tyr Gln Asn Val Ser Ser Ala Met His Ala Phe Ala Pro
 565 570 575
 Gln Gln Gln Phe His Leu Pro Gln His Tyr Lys Thr Asn Thr Ser Val
 580 585 590
 Pro Gln Asn Asp Ser Thr Ser Val Phe Pro Leu Pro Asn Asn Asn Asn
 595 600 605

Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
 610 615 620
 Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
 625 630 635 640
 Thr Pro Thr Val Ser Gln Pro Ser Ser Lys Cys Thr Ser Ser Ser Ser
 645 650 655
 Thr Thr Pro Asn Ile Thr Thr Thr Ile Gln Pro Lys Arg Lys Gln Arg
 660 665 670
 Val Gly Lys Thr Lys Thr Lys Glu Ser Arg Lys Val Ala Ala Ala Gln
 675 680 685
 Lys Val Met Lys Ser Lys Lys Leu Glu Gln Asn Gly Asp Ser Ala Ala
 690 695 700
 Thr Asn Phe Ile Asn Val Thr Pro Lys Asp Ser Gly Gly Lys Gly Thr
 705 710 715 720
 Val Lys Val Gln Asn Ser Asn Ser Gln Gln Gln Leu Asn Gly Ser Phe
 725 730 735
 Ser Met Asp Thr Glu Thr Phe Asp Ile Phe Asn Ile Gly Asp Phe Ser
 740 745 750
 Pro Asp Leu Met Asp Ser
 755

<210> 32
 <211> 750
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 32
 Met Thr Ser Val Asn Arg Ser Asn Asn Thr Arg Ser Met Ser Ala Ser
 1 5 10 15
 Arg Ser Ala Thr Ser Arg Val Arg Asn Thr Thr Ala Asn Ser Ser Asp
 20 25 30
 Val Asn Ser Ser Lys Arg Asn Ser Asn Ser Val Tyr Asp Asp Asn Ser
 35 40 45
 Ser Lys Arg Arg Ser Arg Arg Ser Asp Gly Lys Asn Asn Asp His Thr
 50 55 60
 Tyr Arg Thr Thr Val Lys Ser Lys Asn Ser Arg Tyr Val Ser Ser Ser
 65 70 75 80
 Lys Arg Ala Lys Arg Asn Ser Val Gly Thr Ser Ser Ala Ser Lys Ser
 85 90 95
 Ser Asn Gly Gly Ser Ala His Lys Trp Ser Asn Met Lys Asn Val Ser
 100 105 110
 Asn Ser Ala Val Asp Ala Gly Ser Asp Ser Lys Ser Val Gly Gly Arg
 115 120 125
 Lys Ser Asn Asn Ser Asn Asp Lys Asp Asn Ser Ala Arg Asp Asp Asn
 130 135 140

Asn	Ser	Gly	Asn	Asn	Asn	Asn	Asn	Asn	Asn	His	Ser	Ser	Asn	Asn	Asn	
145					150					155						160
Asp	Asn	Asn	Asn	Asn	Asn	Asn	Asp	Asp	Asn	Asn	Asn	Asn	Asn	Asn	Ser	
				165				170							175	
Asn	Ser	Arg	Asp	Asn	Asn	Asn	Asn	Ser	Asp	Asp	Ser	Asn	Arg	Asn	Asp	
			180					185					190			
Ser	Cys	Lys	Ala	Ser	Asn	Lys	Arg	Ser	Gly	Ala	Lys	Tyr	Lys	Val	Val	
		195					200					205				
Lys	Arg	Cys	Ser	Thr	Asn	Ser	Thr	Thr	Lys	Ser	Trp	Thr	Tyr	Lys	Asn	
	210					215					220					
Thr	Asp	Val	Asn	Asn	Tyr	Val	Thr	Thr	Thr	Ala	Ser	His	Asp	Val	Gly	
225					230					235					240	
Val	Tyr	Arg	Arg	Arg	Trp	Val	Tyr	Gly	Thr	Thr	Asp	Val	Lys	Asn	Ser	
				245					250					255		
Asn	Met	Asp	Val	Cys	Cys	Thr	His	Val	Val	Ser	Ser	Thr	Met	Ser	Asp	
			260					265					270			
Ser	Lys	Tyr	Ser	Thr	Trp	Arg	Gly	Asp	Ser	Arg	Met	Ala	Ala	Tyr	Ser	
		275					280					285				
Ser	Asp	Trp	Lys	Ser	Ala	His	Trp	Tyr	Thr	Ala	Met	Lys	Tyr	Tyr	Asn	
	290					295					300					
His	Gly	Lys	Tyr	Tyr	His	Met	Ser	Thr	Val	Asn	Thr	Ala	Val	Asn	Gly	
305					310					315					320	
Lys	Ser	Val	Cys	Thr	Thr	Ser	Tyr	Met	Val	Asp	Asn	Tyr	Arg	Ala	Val	
				325					330					335		
Arg	Asn	Asn	Gly	Asn	Arg	Asn	Ser	Tyr	Lys	His	Ser	Ala	Met	Ser	Ser	
			340					345					350			
Asp	Asn	Val	Val	Ser	Tyr	Lys	Gly	Asp	Ala	Asn	Gly	Cys	Asn	Asn	Ala	
		355					360					365				
Asp	Met	Val	Asn	Asp	Lys	Tyr	Arg	His	Gly	Ser	Ala	Ser	His	Val	Gly	
	370					375					380					
Gly	Lys	Asn	Ala	Lys	Tyr	Lys	Arg	Lys	Asp	Lys	Lys	Arg	Lys	Lys	Ser	
385					390					395					400	
Ser	Asn	Asn	Asp	Ser	Ser	Val	Thr	Ser	Ser	Thr	Gly	Asn	Ser	Arg	Asn	
				405					410					415		
Asp	Asn	Asp	Asp	Asp	Met	Ser	Ser	Thr	Thr	Ser	Ser	Asp	His	Asp	Ala	
				420				425					430			
Asn	Asp	Asp	Thr	Arg	Arg	Ser	Met	Thr	Asn	Ala	Trp	Thr	Lys	Asn	Met	
		435					440					445				
Thr	Ser	Lys	Cys	Gly	Val	Arg	Lys	His	Gly	Gly	Ala	His	Trp	Tyr	Ser	
	450					455					460					
Cys	Lys	Ser	Ser	Ser	Asp	Val	Ser	Lys	Trp	Met	Val	Lys	Arg	Ala	Trp	
465					470					475					480	

Asp Thr Met Val Thr Met Asn Val Val Tyr Asp Asn Thr Ser Asn Ser
 485 490 495
 Gly Asp Cys Asp Asp Tyr Asp Lys Ser Ser Asn Gly Gly Cys Trp Gly
 500 505 510
 Thr Trp Asp Thr Cys Lys Asn Thr His Ser Ser Ser Asp Asn Gly Lys
 515 520 525
 Asp Tyr Met Ala Asp Ser Thr Asp Gly Asp Lys Asp Asn Gly Lys Trp
 530 535 540
 Lys Arg Ala Cys Arg Thr Arg Ser Arg Ser Gly Val Arg Asn Asp Tyr
 545 550 555
 Arg Ser Ser Asn Thr Asn Gly Ser Val Lys Cys Asn His Asn Asn Val
 565 570 575
 Gly Ala Ser Asp Ser Ala Arg Ser Asn Asn Thr Asp His Ala Val Ser
 580 585 590
 Val Asn Gly Asp Asn His Tyr Val Gly Tyr Lys Lys Arg Ala Asp Tyr
 595 600 605
 Thr Cys Asp Lys Asn Gly Ser Ala Ser Tyr Thr Thr Trp Tyr Val Asn
 610 615 620
 Ser Asn Asn Thr Asn Asp Asn Asn Tyr Asn Ser Lys Asn Gly Cys Lys
 625 630 635 640
 Ser Asp Tyr Asp Lys Thr Thr Tyr Val Asp Ala Thr Ser Trp Arg His
 645 650 655
 Ser Ala Arg Lys Ala Asn Arg Arg Ala Cys Thr Thr Arg Arg Lys Ser
 660 665 670
 Lys Asp Asn Val Met Ala Ala Thr Arg Gly Thr Arg Tyr Tyr Asn Lys
 675 680 685
 Val Arg Thr Gly Asn Val Ala Thr His Asn Thr Trp Arg Thr His Val
 690 695 700
 Asp Val Ser Val Met Lys Ala Lys Ser Ala Ser Arg Ser Arg Arg Asn
 705 710 715 720
 Tyr Val Val Ser Asp Asp Asp Ala Met Lys Lys Lys Ala Lys Lys Thr
 725 730 735
 Ser Thr Arg Val Ser Cys Thr Lys Gly Arg His Cys Thr Asp
 740 745 750

<210> 33

<211> 710

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 33

Met Asp Asn Lys Arg Tyr Asn Gly Asn Ser Asn Val Asp Gly Thr Tyr
 1 5 10 15

Asp Arg Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val
 20 25 30

Ser Asp Lys Arg Gly Arg Ser Ser Ser Thr Ser Lys Gly Ser Tyr Arg
 35 40 45
 Thr Arg Ala Gly Arg Ser Asp Thr Thr Asn Ser Ser Ala Lys His His
 50 55 60
 Ser Lys Lys Ser Thr Val Val Val Val Thr Ser Ser Thr Asp Ser Asn
 65 70 75 80
 Ser Thr Thr Tyr Ala Arg Val Ser Ser Asp Ser Thr Val Ala Thr Ser
 85 90 95
 Ser Thr Thr Thr Arg Thr Arg Thr Arg Asn Asn Thr Val Ser Ser Thr
 100 105 110
 Ala Ser Ser Ser Thr Thr Asp Val Gly Asn Ala Thr Ser Ala Asn Trp
 115 120 125
 Ser Ala Asn Ala Ser Asn Thr Ser Ser Ser Asp Tyr Ala Thr Ser Tyr
 130 135 140
 Thr Arg Lys Ser Thr Asp Asn Tyr Thr Thr Ala Asn Ser Lys Asn Gly
 145 150 155 160
 Asn Asn Trp Ser Ser Ala Gly Asn Ser Asn Thr Asp His Asn Thr Val
 165 170 175
 Asn Arg Arg Ser Ser Thr Thr Asn Arg Val Tyr Thr Asp Ala Tyr
 180 185 190
 Tyr Ala Asn Tyr Val Val Arg Val Lys Ser Thr Ser Ser Val Asp Asp
 195 200 205
 Val Asp Ala Ser Asn Trp Thr Ala Asn Lys Val Val Asn Ser Ala Thr
 210 215 220
 Asn Thr Ser Ser Asn Val Thr His Asn Ala Val Asn Thr Ser Thr Ser
 225 230 235 240
 Ala Thr Cys Ser Tyr Gly Lys Val Ser Ala Arg Thr Arg Gly Asn Met
 245 250 255
 Ala Val Ser Thr Val Ser Ala Cys Ala Ala Gly Lys Ser Lys Val Gly
 260 265 270
 Ala Ser Thr Val Ser Ala Arg Val Met Tyr Asn Val Asn Gly Asn Asn
 275 280 285
 Thr Lys Asn His Gly Val Asn Tyr Ser Thr Ser Asn Asn Thr Tyr Cys
 290 295 300
 Asn Thr Asn Ser His Ser Ser Asn Asn Tyr Ser Ser Asp Ser Lys Lys
 305 310 315 320
 Asp His Thr Ser Ser Lys Tyr Asp His Asn His Asn Ala Lys Asn Lys
 325 330 335
 Gly Val Ser Asp Thr Asn Tyr Gly His Asn Ser Lys Val Lys Arg Lys
 340 345 350
 Asp Thr Asp Ala Lys Arg Arg Lys Asp Ser Asn Ser Ser Thr Met Ala
 355 360 365

Val	Met	Asp	Ser	Ser	Asp	Tyr	Gly	Asn	Thr	Val	Lys	Asn	Ser	Ser	Asn	
370						375					380					
Arg	Asp	Met	Arg	Lys	Cys	Asn	Lys	Tyr	Thr	Ser	Met	Gly	Val	His	Lys	
385					390					395					400	
Asn	Gly	Thr	Trp	Val	Cys	Lys	Lys	Met	Ala	Asn	Thr	Arg	Asn	Val	Thr	
				405					410					415		
Ser	Gly	Val	Ser	Asp	Tyr	Cys	Thr	Asn	Asp	Gly	Asn	Tyr	Val	Gly	Lys	
			420					425					430			
Gly	Trp	Asn	Ser	Ser	Val	Ser	His	Trp	Thr	Val	Asn	Arg	Tyr	Gly	Ser	
		435					440					445				
Arg	Ala	Val	Arg	Ala	Cys	Ala	Asp	Ser	Thr	Cys	Thr	Thr	Ser	Val	Ser	
	450					455					460					
Tyr	Ala	Thr	Asp	Thr	Asn	Gly	Thr	Thr	Trp	Asp	Thr	Cys	Thr	Asn	Lys	
465					470					475					480	
Asn	Cys	Asp	Lys	Val	Asn	Lys	Asn	Val	Lys	Cys	Cys	His	Lys	Gly	Ser	
				485					490					495		
Thr	Val	Lys	Asn	Arg	Gly	Gly	Ala	Ser	Lys	Asn	Lys	His	Ala	Asp	Gly	
			500					505					510			
Ser	Ser	Asp	Ser	Asp	Gly	Asn	Tyr	Gly	Thr	Tyr	Lys	Val	Thr	Ser	Arg	
		515					520					525				
Asp	Asn	Ser	Val	Arg	Asp	Ala	Thr	Lys	Arg	Asn	Ser	Asn	Asn	Ser	Arg	
	530					535					540					
Val	Gly	Ser	Ser	Ala	Gly	Ser	Lys	Ser	Ser	Lys	Asn	His	Arg	Lys	His	
545					550					555					560	
Gly	His	Ser	Gly	Arg	Ala	Arg	Gly	Val	Ser	Val	Ser	Ser	Val	Arg	Ser	
				565				570						575		
Ser	Asn	Ser	Arg	His	Asn	Ser	Val	Met	Asn	Asn	Ala	Gly	Thr	Ala	Asn	
			580					585					590			
Asn	Ala	Met	Ser	Asn	Ser	Tyr	Asn	Asn	Val	Val	Tyr	Ser	Gly	Asn	Asn	
		595					600					605				
Asn	Asn	Gly	Asn	Ser	Asn	Gly	Asp	Asn	Ser	Asp	Ser	Arg	Ala	Asn	Gly	
	610					615					620					
Thr	Asn	Ser	Val	Asn	Asn	Val	Ser	Asn	Asn	Asn	Asn	Asn	Tyr	Asn	Asn	
625					630					635					640	
Ser	Gly	Tyr	Ser	Ser	Met	Asn	Ser	Arg	Ser	Val	Ser	His	Asn	Asn	Asn	
				645					650					655		
Asn	Asn	Thr	Asn	Asn	Tyr	Asn	Asn	Asn	Asp	Asn	Asp	Asn	Asn	Asn	Asn	
			660					665					670			
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
	675						680					685				
Asn	Ser	Asn	Asn	Ser	Asn	Asn	Asn	Asn	Asn	Asn	Asp	Thr	Ser	Tyr	Arg	
	690					695					700					

Tyr Arg Ser Tyr Gly Tyr
705 710

<210> 34
<211> 477
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 34
Asp Thr Lys Gly Tyr Asp Asp Asp Ala Ala Thr Asp Gly Lys Lys His
1 5 10 15
Arg Arg Tyr Arg Tyr Val Ser Gly Ser Val Ser Gly Lys Arg Trp Thr
20 25 30
Asp Gly Val Ser Trp Ser Ser Arg Ser Gly Lys Tyr Lys Asp Lys Asn
35 40 45
Ala Gly Ser Asn Ala Asn Ala Thr Ser Ser Gly Ser Thr Asp Ser Ala
50 55 60
Val Thr Asp Gly Thr Ser Gly Ala Arg Asn Asn Ser Ser Ser Lys Lys
65 70 75 80
Lys Asn His Asp Thr Met Gly His Ser Ser Ser Asp Thr Ser Ser Ser
85 90 95
Asn Arg Ser Asn Lys Tyr Thr Gly Val Lys Lys Thr Ser Val Lys Lys
100 105 110
Arg Asn Ser Asn His Val Ser Tyr Tyr Ser Val Lys Asp Lys Asn Cys
115 120 125
Val Thr Lys Ala Ser Lys Asp Val Arg Ser Val Ala Met Gly Asn Thr
130 135 140
Thr Gly Asn Val Lys Asn Asn Ser Thr Thr Thr Gly Asn Gly Asn Asn
145 150 155 160
Asn Asn Lys Ser Asn Ser Ser Thr Asn Thr Val Ser Thr Asn Asn Asn
165 170 175
Ser Ala Asn Asn Ala Ala Gly Ser Asn Thr Ser Ala Asn Lys Asn Tyr
180 185 190
Tyr Tyr Lys Asn Asp Ser Ser Gly Tyr Thr Ala Ala Ser Thr Thr Met
195 200 205
Tyr Thr Ala Asn Tyr Thr Ser Asp Asn Thr Asn Ala Thr Gly Met Asn
210 215 220
Thr His Val Asn Asn Asn Asn Asn Asn Ser Asn Asn Ser Ser Asn Ser
225 230 235 240
Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
245 250 255
Asn Asn Asn Asn Asn Asn Asn Asn Val Asn Thr Asn Ala Gly Asn Gly
260 265 270
Asn Asn Asn Arg His Asn Ala Ser Ala Tyr Asn Thr Thr Gly Asp Asn
275 280 285

Gly Ser Tyr Tyr Tyr Thr Thr Asn Asn Asn Tyr Tyr Thr Thr Asn Val
 290 295 300
 Thr Asn Ala Ser Thr Asn Asn Gly Tyr Ser Thr Ser Ser Thr His Tyr
 305 310 315 320
 Tyr Gly His Thr Ser Ser Ala Ser Ala Ala Gly Ala Thr Gly Thr
 325 330 335
 Gly Thr Ala Asn Val Val Ser Ser Met His Ala Asn Asn Asn Ser Ala
 340 345 350
 Ser Ser Ala Thr Ser Thr Ala Tyr Val Tyr Ser Met Asn Val Asn Val
 355 360 365
 Tyr Tyr Asn Ser Ser Ala Ser Ala Tyr Lys Arg Ala Asn Thr Thr Ser
 370 375 380
 Asn Thr Asn Ala Ser Gly Ala Thr Ser Thr Asn Ser Gly Thr Met Ser
 385 390 395 400
 Asn Ala Tyr Ala Asn Ser Tyr Thr Ser Val Tyr Tyr Gly Tyr Ala Met
 405 410 415
 Ala Ser Ala Asn Ser Met Tyr His His His Thr Val Tyr Ala Thr Asn
 420 425 430
 Met Ser Ser Gly His Thr Ser Thr Gly Ser Asp His His His Tyr Asn
 435 440 445
 Asp His Lys Asn Ala Met Gly His Ala Asn Asn Asn Asn Thr Asn Asn
 450 455 460
 Asp Thr Met Asn Asn Asn Thr Asn Thr Ser Thr Thr Thr
 465 470 475

<210> 35
 <211> 454
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 35
 Met Asp Val Arg Ala Ala Cys Ser Ala Ser Gly Arg Thr Gly Lys Lys
 1 5 10 15
 Gly Tyr Ser Tyr Lys Met Ser Asn Ser Gly Gly Ser Ser Ser Gly Gly
 20 25 30
 Ser Asp Val Gly Ser Thr Asn Gly Ser Asn Arg Ala Lys Asn Thr Asn
 35 40 45
 Tyr Lys Lys Thr Asn Lys Lys Tyr Lys Ala Thr Asp Lys Ala Asn Asp
 50 55 60
 Thr Lys Tyr Tyr Ser Asn Asp Lys Lys Ser Lys Arg Ser Ala Asn Ser
 65 70 75 80
 Met Asn Asp Lys Asp Lys Cys Arg Thr Thr Asn Lys Asp Met Thr Arg
 85 90 95
 Tyr Asp Ser Lys Ser Lys Val Thr Asn Cys Asp His Lys Ala Ser Ser
 100 105 110

His Ser Met Lys Tyr Lys Lys Arg Ser Val Asp Lys Asp His Val Met
 115 120 125
 Lys Asp Asp Ser Ser Val Lys Ala Ser Lys Met Asn Ser His Asn Tyr
 130 135 140
 Ser Thr Asn Thr Met Asn Lys Met Asp Val Tyr Thr Lys Ala Asn Met
 145 150 155 160
 Ala Asn Lys Lys Lys Ser Asp Thr Ser Thr Trp Lys Asn Lys Asn Lys
 165 170 175
 Ser His Val Ser Tyr Asn Asn Asp Lys Ser Lys Thr Lys Trp Tyr Asn
 180 185 190
 Asp Ser Asp Asp Asp Asp Asp Asn Asn Val Asn Asn Asn Asp Asn Asn
 195 200 205
 Asn Asn Asn Lys Asn Asp Asn Asn Asn Asp Asn Asn Asn Asp Thr Ser
 210 215 220
 Asn Asn Asn Asn Asn Asn Asn Asn Arg Thr Lys Asn Asn Arg Asn Asn
 225 230 235 240
 Arg Asp Trp Lys Thr Lys Lys Cys Thr Asp Met Asn Asp Lys Arg Asp
 245 250 255
 Asn Asn Asn Lys Asn Asp Met Ala Arg Asn Asp Asn Lys Asn Tyr Asn
 260 265 270
 Asn Val Asn Lys Arg Asn His Lys Ser Ser Cys Arg Arg Asp Gly Tyr
 275 280 285
 Ser Ala Asn Asn Ala Val Asn Ser Thr His Ala Ser Asn Lys Asn Val
 290 295 300
 Asn Asp Met Asn Asn Asp Thr Tyr Lys Asn Lys Thr Asp Thr Asn Lys
 305 310 315 320
 Lys Asn Asp Ser Asn Ser Asn Asp Val Thr Arg Lys Lys Arg Lys Thr
 325 330 335
 Ser Asp Gly Asn Tyr Ser Arg Asn Asn Val Ser Val Ser Arg Ser Lys
 340 345 350
 Ala Thr Thr Lys Lys Thr Lys Lys Lys Lys Arg Arg Asp Gly Lys Asp
 355 360 365
 Lys Lys Asn Lys Lys Asn Ala Asp Asn Lys Lys Asn Asn Ala Val Thr
 370 375 380
 Val Ser Val Tyr Asp Ser Asn Lys Val Lys Ser Asn Lys Arg Ser Arg
 385 390 395 400
 Lys Val Asn Asn Lys Ser Asp Val Val Asn Ser Gly Lys Asp Ser Arg
 405 410 415
 Val Lys Ser Cys Lys Lys Tyr Ala Asp Asn Asn Thr Lys Ser Asn Asp
 420 425 430
 Ala Asp Gly Trp Asp Asp Met Asn Trp Val Asp Arg Gly Cys Ala Thr
 435 440 445

Thr Arg Trp Arg Ala Lys
450

<210> 36
<211> 284
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 36

Met	Asn	Val	Thr	Ser	Lys	Asp	Gly	Asn	His	Ser	Ser	Lys	Lys	Asn	Arg
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Asn	Thr	Asn	Lys	Arg	His	Lys	Asn	Ala	Ser	Asn	Asp	Arg	Asp	Ser	Val
		20						25					30		
Ser	Ser	Asn	Thr	Thr	Ser	Met	Thr	Asp	Asp	Ala	Asp	Tyr	Asn	Gly	Ala
		35					40					45			
Ser	Arg	Thr	Lys	Asn	Asn	Ser	Asp	Ser	Asp	Arg	Ser	Asn	Asp	Thr	Lys
	50					55					60				
Asn	Asn	Tyr	Asn	Lys	Arg	Thr	Gly	Tyr	Asn	Tyr	Asn	Gly	Ser	Gly	Asn
65					70					75					80
Arg	Tyr	Thr	Arg	Lys	Arg	Thr	Ala	Asn	Lys	Ala	Tyr	Ser	Asp	Asp	Asn
				85					90					95	
Val	Lys	Asp	Asp	Asn	Asn	Thr	Lys	Lys	Ala	Ser	Arg	Ser	Ser	Gly	Arg
			100					105					110		
Asn	Val	Asn	Thr	Arg	Asn	Lys	Ser	Lys	Ser	His	Lys	Val	Lys	Asn	Asn
		115						120				125			
Lys	Ser	Ser	Ser	Arg	Lys	Ser	Ser	Ala	Ala	Arg	Lys	Gly	Lys	Tyr	Asn
	130					135					140				
Ser	Asn	Ser	Asp	Ser	Thr	Thr	Arg	Lys	Val	Thr	Asp	Val	Lys	Lys	Arg
145					150					155					160
Ser	Lys	Trp	His	Arg	His	Asp	Lys	Lys	Met	Val	Lys	Lys	Ser	Arg	Tyr
				165					170					175	
Arg	Lys	Arg	Met	Arg	Gly	Thr	Asp	Val	Ser	Ser	Ser	Asp	Asn	Ser	Lys
			180					185					190		
Ser	Thr	Thr	Lys	Ser	Tyr	Val	Ser	Lys	Asn	Ser	Ala	Met	Asn	Asn	Asn
		195					200					205			
Asp	Val	Thr	Asp	Asn	Lys	Lys	Thr	Asn	Asn	Asn	Lys	Ala	Arg	Asp	Ser
	210					215					220				
Met	His	Thr	Lys	Lys	Asp	Thr	Lys	Asp	Asp	Thr	Asp	Ser	Lys	Lys	Arg
225					230					235					240
Lys	Val	Val	Thr	Asn	Asp	Asn	Ala	Ala	Met	Val	Asn	Lys	Gly	Trp	Arg
				245					250					255	
Lys	Asn	Val	Met	Met	Tyr	Lys	Lys	Ser	Gly	Asn	Met	Lys	Lys	Tyr	Arg
			260					265					270		
Tyr	Trp	Thr	Cys	Tyr	Cys	Asn	Tyr	Val	Tyr	Tyr	Arg				
		275					280								

<210> 37
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 37
 gggaattccc attaccgaca tttgggcgc 29

<210> 38
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 38
 ggggattctg attgattgat tgattgtac 29

<210> 39
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: superbright
 GFP encoding sequence

<220>
 <221> CDS
 <222> (1)..(720)

<400> 39
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

ggt gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc act tat ggt gtt cag tgc ttt tca aga tac ccg gat cat atg aaa 240
 Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

aga act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
att gat ttt aaa gaa gat gga aac att ctt ggg cac aaa ttg gaa tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
gga atc aaa gct aac ttc aaa att aga cac aac att gaa gat gga agc	528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa tga	720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys	
225 230 235 240	

<210> 40
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<400> 40	
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 41
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
gaccgcggat ggctagcaaa ggagaag

27

<210> 42
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 42
cctgagctct catttgtata gttcatcc

28

<210> 43
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
ggaggatcca tggatacggg taagttaatc tcag

34

<210> 44
<211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
ggaccgcggg tagcggttct gttgagaaaa gttgcc 36

<210> 45
<211> 7239
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: vector
containing chimeric gene

<400> 45
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cttaggacgg atcgcttgcc tgtaacttac acgcgcctcg tatctdddta tgatggaata 120
attdgggaat ttactctgtg tttattdatt tttatgtdtt gtattdggat ttdagaaagt 180
aaataaagaa ggtagaagag ttacggaatg aagaaaaaaa aataaacaaa ggttdtaaaa 240
attdcaacaa aaagcgtact ttacatatat attdattaga caagaaaagc agattaaata 300
gatatacatt cgattaacga taagtaaaat gtaaaatcac aggattdtdg tgtgtggtct 360
tctacacaga caagatgaaa caattdcgga ttaatacctg agagcaggaa gagcaagata 420
aaaggtagta ttdgttdggc atccccctag agtdtdtdac attdtdcgga aacaaaaact 480
attdtdtdct taattdtdtd ttdtacttdt tattdtdaat ttatatattd atattaaaaa 540
attdaaatta taattdtdtd tatagcacgt gatgaaaagg acccaggtgg cacttdtdcg 600
ggaaatgtgc gcggaacccc tattdgttda ttdtdtdtaa tacattcaaa tatgtatccg 660
ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt 720
attcaacatt tccgtgtcgc ccttattdcc ttdtdtdcgga cattdtdgct tctgttdtdt 780
gctcaccag aaacgctggg gaaagtaaaa gatgctgaag atcagtdggg tgcacgagtg 840
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cgtdtdtdcaa tgatgagcac ttdtaagtdt ctgctatgtg gcgcgggtatt atcccgtdatt 960
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<210> 46
 <211> 741
 <212> PRT
 <213> *Pichia pinus*

<400> 46
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 Ala Gly Asn Val Gln Asn Ile Asn Leu Asn Ala Pro Ala Tyr Asp Pro
 20 25 30
 Ala Val Gln Ser Tyr Ile Pro Asn Thr Ala Gln Ala Phe Val Pro Ser
 35 40 45
 Ala Gln Pro Tyr Ile Pro Gly Gln Gln Glu Gln Gln Phe Gly Gln Tyr
 50 55 60
 Gly Gln Gln Gln Gln Asn Tyr Asn Gln Gly Gly Tyr Asn Asn Tyr Asn
 65 70 75 80
 Asn Arg Gly Gly Tyr Ser Asn Asn Arg Gly Gly Tyr Asn Asn Ser Asn
 85 90 95
 Arg Gly Gly Tyr Ser Asn Tyr Asn Ser Tyr Asn Thr Asn Ser Asn Gln
 100 105 110
 Gly Gly Tyr Ser Asn Tyr Asn Asn Asn Tyr Ala Asn Asn Ser Tyr Asn
 115 120 125
 Asn Asn Asn Asn Tyr Asn Asn Asn Tyr Asn Gln Gly Tyr Asn Asn Tyr
 130 135 140
 Asn Ser Gln Pro Gln Gly Gln Asp Gln Gln Gln Glu Thr Gly Ser Gly
 145 150 155 160
 Gln Met Ser Leu Glu Asp Tyr Gln Lys Gln Gln Lys Glu Ser Leu Asn
 165 170 175
 Lys Leu Asn Thr Lys Pro Lys Lys Val Leu Lys Leu Asn Leu Asn Ser
 180 185 190
 Ser Thr Val Lys Ala Pro Ile Val Thr Lys Lys Lys Glu Glu Glu Pro
 195 200 205
 Val Asn Gln Glu Ser Lys Thr Glu Glu Pro Ala Lys Glu Glu Ile Lys
 210 215 220
 Asn Gln Glu Pro Ala Glu Ala Glu Asn Lys Val Glu Glu Glu Ser Lys
 225 230 235 240
 Val Glu Ala Pro Thr Ala Ala Lys Pro Val Ser Glu Ser Glu Phe Pro
 245 250 255
 Ala Ser Thr Pro Lys Thr Glu Ala Lys Ala Ser Lys Glu Val Ala Ala
 260 265 270

Ala	Ala	Ala	Ala	Leu	Lys	Lys	Glu	Val	Ser	Gln	Ala	Lys	Lys	Glu	Ser
		275					280					285			
Asn	Val	Thr	Asn	Ala	Asp	Ala	Leu	Val	Lys	Glu	Gln	Glu	Glu	Gln	Ile
	290					295					300				
Asp	Ala	Ser	Ile	Val	Asn	Asp	Met	Phe	Gly	Gly	Lys	Asp	His	Met	Ser
305					310					315					320
Ile	Ile	Phe	Met	Gly	His	Val	Asp	Ala	Gly	Lys	Ser	Thr	Met	Gly	Gly
				325					330					335	
Asn	Leu	Leu	Phe	Leu	Thr	Gly	Ala	Val	Asp	Lys	Arg	Thr	Val	Glu	Lys
			340					345					350		
Tyr	Glu	Arg	Glu	Ala	Lys	Asp	Ala	Gly	Arg	Gln	Gly	Trp	Tyr	Leu	Ser
		355					360					365			
Trp	Ile	Met	Asp	Thr	Asn	Lys	Glu	Glu	Arg	Asn	Asp	Gly	Lys	Thr	Ile
	370					375					380				
Glu	Val	Gly	Lys	Ser	Tyr	Phe	Glu	Thr	Asp	Lys	Arg	Arg	Tyr	Thr	Ile
385					390					395					400
Leu	Asp	Ala	Pro	Gly	His	Lys	Leu	Tyr	Ile	Ser	Glu	Met	Ile	Gly	Gly
				405					410					415	
Ala	Ser	Gln	Ala	Asp	Val	Gly	Val	Leu	Val	Ile	Ser	Ser	Arg	Lys	Gly
			420					425					430		
Glu	Tyr	Glu	Ala	Gly	Phe	Glu	Arg	Gly	Gly	Gln	Ser	Arg	Glu	His	Ala
		435					440					445			
Ile	Leu	Ala	Lys	Thr	Gln	Gly	Val	Asn	Lys	Leu	Val	Val	Val	Ile	Asn
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<211> 653

<212> DNA

<213> *Saccharomyces cerevisiae*

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ure2N-Sup35C
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 Tyr Gly Arg Pro Gln Tyr Gly Gly Asn Gln Asn Ser Asn Gly Gln His
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 Glu Ser Phe Asn Phe Ser Gly Asn Phe Ser Gln Gln Asn Asn Asn Gly
 385 390 395 400
 Asn Gln Asn Arg Tyr
 405

<210> 51
 <211> 128
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 51
 Met Ser Ala Asn Asp Tyr Tyr Gly Gly Thr Ala Gly Glu Lys Ser Gln
 1 5 10 15

Tyr Ser Arg Pro Ser Asn Pro Pro Pro Ser Ser Ala His Gln Asn Lys
 20 25 30
 Thr Gln Glu Arg Gly Tyr Pro Pro Gln Gln Gln Gln Tyr Tyr Gln
 35 40 45
 Gln Gln Gln Gln His Pro Gly Tyr Tyr Asn Gln Gln Gly Tyr Asn Gln
 50 55 60
 Gln Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln
 65 70 75 80
 Gly Tyr Asn Gln Gln Gly Tyr Asn Gln Gln Gly His Gln Gln Pro Val
 85 90 95
 Tyr Val Gln Gln Gln Pro Pro Gln Arg Gly Asn Glu Gly Cys Leu Ala
 100 105 110
 Ala Cys Leu Ala Ala Leu Cys Ile Cys Cys Thr Met Asp Met Leu Phe
 115 120 125

<210> 52
 <211> 534
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 52
 Met Ser Ser Asp Glu Glu Asp Phe Asn Asp Ile Tyr Gly Asp Asp Lys
 1 5 10 15
 Pro Thr Thr Thr Glu Glu Val Lys Lys Glu Glu Glu Gln Asn Lys Ala
 20 25 30
 Gly Ser Gly Thr Ser Gln Leu Asp Gln Leu Ala Ala Leu Gln Ala Leu
 35 40 45
 Ser Ser Ser Leu Asn Lys Leu Asn Asn Pro Asn Ser Asn Asn Ser Ser
 50 55 60
 Ser Asn Asn Ser Asn Gln Asp Thr Ser Ser Ser Lys Gln Asp Gly Thr
 65 70 75 80
 Ala Asn Asp Lys Glu Gly Ser Asn Glu Asp Thr Lys Asn Glu Lys Lys
 85 90 95
 Gln Glu Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn Ala Ser Ser Ala
 100 105 110
 Gly Pro Ser Gly Leu Pro Trp Glu Gln Leu Gln Gln Thr Met Ser Gln
 115 120 125
 Phe Gln Gln Pro Ser Ser Gln Ser Pro Pro Gln Gln Gln Val Thr Gln
 130 135 140
 Thr Lys Glu Glu Arg Ser Lys Ala Asp Leu Ser Lys Glu Ser Cys Lys
 145 150 155 160
 Met Phe Ile Gly Gly Leu Asn Trp Asp Thr Thr Glu Asp Asn Leu Arg
 165 170 175

Glu	Tyr	Phe	Gly	Lys	Tyr	Gly	Thr	Val	Thr	Asp	Leu	Lys	Ile	Met	Lys	
			180					185					190			
Asp	Pro	Ala	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe	Leu	Ser	Phe	Glu	
		195					200					205				
Lys	Pro	Ser	Ser	Val	Asp	Glu	Val	Val	Lys	Thr	Gln	His	Ile	Leu	Asp	
	210					215					220					
Gly	Lys	Val	Ile	Asp	Pro	Lys	Arg	Ala	Ile	Pro	Arg	Asp	Glu	Gln	Asp	
225					230					235					240	
Lys	Thr	Gly	Lys	Ile	Phe	Val	Gly	Gly	Ile	Gly	Pro	Asp	Val	Arg	Pro	
			245						250					255		
Lys	Glu	Phe	Glu	Glu	Phe	Phe	Ser	Gln	Trp	Gly	Thr	Ile	Ile	Asp	Ala	
			260					265					270			
Gln	Leu	Met	Leu	Asp	Lys	Asp	Thr	Gly	Gln	Ser	Arg	Gly	Phe	Gly	Phe	
		275					280					285				
Val	Thr	Tyr	Asp	Ser	Ala	Asp	Ala	Val	Asp	Arg	Val	Cys	Gln	Asn	Lys	
	290					295					300					
Phe	Ile	Asp	Phe	Lys	Asp	Arg	Lys	Ile	Glu	Ile	Lys	Arg	Ala	Glu	Pro	
305					310					315					320	
Arg	His	Met	Gln	Gln	Lys	Ser	Ser	Asn	Asn	Gly	Gly	Asn	Asn	Gly	Gly	
			325						330					335		
Asn	Asn	Met	Asn	Arg	Arg	Gly	Gly	Asn	Phe	Gly	Asn	Gln	Gly	Asp	Phe	
			340					345					350			
Asn	Gln	Met	Tyr	Gln	Asn	Pro	Met	Met	Gly	Gly	Tyr	Asn	Pro	Met	Met	
		355					360					365				
Asn	Pro	Gln	Ala	Met	Thr	Asp	Tyr	Tyr	Gln	Lys	Met	Gln	Glu	Tyr	Tyr	
	370					375					380					
Gln	Gln	Met	Gln	Lys	Gln	Thr	Gly	Met	Asp	Tyr	Thr	Gln	Met	Tyr	Gln	
385					390					395					400	
Gln	Gln	Met	Gln	Gln	Met	Ala	Met	Met	Met	Pro	Gly	Phe	Ala	Met	Pro	
			405						410					415		
Pro	Asn	Ala	Met	Thr	Leu	Asn	Gln	Pro	Gln	Gln	Asp	Ser	Asn	Ala	Thr	
			420					425					430			
Gln	Gly	Ser	Pro	Ala	Pro	Ser	Asp	Ser	Asp	Asn	Asn	Lys	Ser	Asn	Asp	
		435					440					445				
Val	Gln	Thr	Ile	Gly	Asn	Thr	Ser	Asn	Thr	Asp	Ser	Gly	Ser	Pro	Pro	
	450					455					460					
Leu	Asn	Leu	Pro	Asn	Gly	Pro	Lys	Gly	Pro	Ser	Gln	Tyr	Asn	Asp	Asp	
465					470					475					480	
His	Asn	Ser	Gly	Tyr	Gly	Tyr	Asn	Arg	Asp	Arg	Gly	Asp	Arg	Asp	Arg	
			485						490					495		
Asn	Asp	Arg	Asp	Arg	Asp	Tyr	Asn	His	Arg	Ser	Gly	Gly	Asn	His	Arg	
			500					505					510			

Arg Asn Gly Arg Gly Gly Arg Gly Gly Tyr Asn Arg Arg Asn Asn Gly
515 520 525

Tyr His Pro Tyr Asn Arg
530

<210> 53
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 53
ggaggatcca tggatacgga taagttaatc tcag 34

<210> 54
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 54
ccaagctttc agtagcgggt ctggtgagaa aagttg 36

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 55
ggtgtcttgg ccaattgccc 20

<210> 56
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
gtcgacctgc agcgtacgca tttcagatct ttgctatac 39

<210> 57
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
 cgagctcgaa ttcacgcgatt gattcagttc gccttctatc 40

<210> 58
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 58
 ctgttttgaa aggggccaca tg 22

<210> 59
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 59
 ggaggatcca tggatacgga taagttaatc tcag 34

<210> 60
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 60
 ggaccgcggg tagcggttct gttgagaaaa gttgcc 36

<210> 61
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 61
 gaggatccat gcctgatgat gaggaagaag acgagg 36

<210> 62
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 62
 cggaattcct cgagaagata tccatc 26

<210> 63
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 63
 gggatcctgt tgctagtggg caga 24

<210> 64
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 64
 gtaccgcgga tgtctttgaa cgactttcaa aagc 34

<210> 65
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 65
 gtggagctct tactcggcaa ttttaacaat ttac 35

<210> 66
 <211> 3153
 <212> DNA
 <213> Saccharomyces cerevisia

<400> 66
 atgtcggatt caaccaagg caacaatcag caaaactacc agcaatacag ccagaacggt 60
 aaccaacaac aaggtaacaa cagataccaa gggtatcaag cttacaatgc tcaagcccaa 120
 cctgcaggtg ggtactacca aaattaccaa gggtattctg ggtaccaaca aggtggctat 180
 caacagtaca atcccgcgc cggttaccag caacagtata atcctcaagg aggctatcaa 240
 cagtacaatc ctcaaggcgg ttatcagcag caattcaatc cacaagggtg ccgtggaaat 300
 tacaaaaact tcaactacaa taacaatttg caaggatata aagctgggtt ccaaccacag 360
 tctcaaggta tgtctttgaa cgactttcaa aagcaacaaa agcaggccgc tcccaaacca 420
 aagaagactt tgaagcttgt ctccagttcc ggtatcaagt tggccaatgc taccaagaag 480
 gttggcacia aacctgccga atctgataag aaagaggaag agaagtctgc tgaaacaaaa 540
 gaaccaacta aagagccaac aaaggctcga gaaccagtta aaaaggagga gaaaccagtc 600
 cagactgaag aaaagacgga ggaaaaatcg gaacttccaa aggtagaaga ccttaaaatc 660

tctgaatcaa	cacataatac	caacaatgcc	aatgttacca	gtgctgatgc	cttgatcaag	720
gaacaggaag	aagaagtgga	tgacgaagtt	gttaacgatc	cgcggatgga	ctccaaagaa	780
tccttagctc	cccctggtag	agacgaagtc	cctggcagtt	tgcttggcca	agggaggggg	840
agcgtaatgg	acttttataa	aagcctgagg	ggaggagcta	cagtcaaggt	ttctgcatct	900
tcgccctcag	tggctgctgc	ttctcaggca	gattccaagc	agcagaggat	tctccttgat	960
ttctcgaaag	gctccacaag	caatgtgcag	cagcgacagc	agcagcagca	gcagcagcag	1020
cagcagcagc	agcagcagca	gcagcagcag	cagccaggct	tatccaaagc	cgtttcactg	1080
tccatggggc	tgtatatggg	agagacagaa	acaaaagtga	tggggaatga	cttgggctac	1140
ccacagcagg	gccaaacttg	cctttcctct	ggggaaacag	actttcggct	tctggaagaa	1200
agcattgcaa	acctcaatag	gtcgaccagc	gttcagaga	acccaagag	ttcaacgtct	1260
gcaactgggt	gtgctacccc	gacagagaag	gagtttccca	aaactcactc	ggatgcatct	1320
tcagaacagc	aaaatcgaaa	aagccagacc	ggcaccaacg	gaggcagtgt	gaaattgtat	1380
cccacagacc	aaagcacctt	tgacctcttg	aaggatttgg	agttttccgc	tgggtcccca	1440
agtaaagaca	caaacgagag	tccctggaga	tcagatctgt	tgatagatga	aaacttgctt	1500
tctcctttgg	cgggagaaga	tgatccattc	cttctcgaag	ggaacacgaa	tgaggattgt	1560
aagcctctta	ttttaccgga	cactaaacct	aaaattaagg	atactggaga	tacaatctta	1620
tcaagtccca	gcagtgtggc	actaccccaa	gtgaaaacag	aaaaagatga	tttcattgaa	1680
ctttgcaccc	ccggggtaat	taagcaagag	aaactgggcc	cagtttattg	tcaggcaagc	1740
ttttctggga	caaataataa	tggtataaaa	atgtctgcca	tttctgttca	tgggtgtgagt	1800
acctctggag	gacagatgta	ccactatgac	atgaatacag	catccctttc	tcagcagcag	1860
gatcagaagc	ctgtttttta	tgtcattcca	ccaattcctg	ttggttctga	aaactggaat	1920
aggtgccaa	gctccggaga	ggacagcctg	acttccttgg	gggctctgaa	cttcccaggc	1980
cggtcagtgt	tttctaattg	gtactcaagc	cctggaatga	gaccagatgt	aagctctcct	2040
ccatccagct	cgtcagcagc	cacgggacca	cctcccaagc	tctgcctggg	gtgctccgat	2100
gaagcttcag	gatgtcatta	cgggggtgctg	acatgtggaa	gctgcaaagt	attctttaaa	2160
agagcagtgg	aaggacagca	caattacctt	tgtgctggaa	gaaacgattg	catcattgat	2220
aaaattcgaa	ggaaaaactg	cccagcatgc	cgctatcgga	aatgtcttca	ggctggaatg	2280
aaccttgaag	ctcgaaaaac	aaagaaaaaa	atcaaaggga	ttcagcaagc	cactgcagga	2340
gtctcacaag	acacttcgga	aaatcctaac	aaaacaatag	ttcctgcagc	attaccacag	2400
ctcacccta	ccttggtgtc	actgctggag	gtgattgaac	ccgaggtgtt	gtatgcagga	2460
tatgatagct	ctgttccaga	ttcagcatgg	agaattatga	ccacactcaa	catgttaggt	2520
gggcgtcaag	tgattgcagc	agtgaaatgg	gcaaaggcga	tactaggctt	gagaaactta	2580

cacctcgatg accaaatgac cctgctacag tactcatgga tgtttctcat ggcatttgcc	2640
ttgggttgga gatcatacag acaatcaagc ggaaacctgc tctgctttgc tcctgatctg	2700
attattaatg agcagagaat gtctctaccc tgcattgatg accaatgtaa acacatgctg	2760
tttgtctcct ctgaattaca aagattgcag gtatcctatg aagagtatct ctgtatgaaa	2820
accttactgc ttctctcttc agttcctaag gaaggtctga agagccaaga gttatttgat	2880
gagattcgaa tgacttatat caaagagcta ggaaaagcca tcgtcaaaaag ggaaggggaac	2940
tccagtcaga actggcaacg gttttaccaa ctgacaaagc ttctggactc catgcatgag	3000
gtgggttgaga atctccttac ctactgcttc cagacatttt tggataagac catgagtatt	3060
gaattcccag agatggttagc tgaaatcatc actaatcaga taccaaaata ttcaaattgga	3120
aatatcaaaa agcttctggt tcatcaaaaa tga	3153

<210> 67
 <211> 1052
 <212> PRT
 <213> Saccharinycees cerevisia

<400> 67

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr	
1 5 10 15	

Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr	
20 25 30	

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn	
35 40 45	

Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn	
50 55 60	

Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln	
65 70 75 80	

Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro Gln Gly	
85 90 95	

Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly	
100 105 110	

Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu Asn Asp	
115 120 125	

Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu	
130 135 140	

Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr Lys Lys
 145 150 155 160

Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu Lys Ser
 165 170 175

Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu Glu Pro
 180 185 190

Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr Glu Glu
 195 200 205

Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu Ser Thr
 210 215 220

His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu Ile Lys
 225 230 235 240

Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp Pro Arg Met
 245 250 255

Asp Ser Lys Glu Ser Leu Ala Pro Pro Gly Arg Asp Glu Val Pro Gly
 260 265 270

Ser Leu Leu Gly Gln Gly Arg Gly Ser Val Met Asp Phe Tyr Lys Ser
 275 280 285

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Val
 290 295 300

Ala Ala Ala Ser Gln Ala Asp Ser Lys Gln Gln Arg Ile Leu Leu Asp
 305 310 315 320

Phe Ser Lys Gly Ser Thr Ser Asn Val Gln Gln Arg Gln Gln Gln Gln
 325 330 335

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro
 340 345 350

Gly Leu Ser Lys Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu
 355 360 365

Thr Glu Thr Lys Val Met Gly Asn Asp Leu Gly Tyr Pro Gln Gln Gly
 370 375 380

Gln Leu Gly Leu Ser Ser Gly Glu Thr Asp Phe Arg Leu Leu Glu Glu
 385 390 395 400

Ser Ile Ala Asn Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys
 405 410 415
 Ser Ser Thr Ser Ala Thr Gly Cys Ala Thr Pro Thr Glu Lys Glu Phe
 420 425 430
 Pro Lys Thr His Ser Asp Ala Ser Ser Glu Gln Gln Asn Arg Lys Ser
 435 440 445
 Gln Thr Gly Thr Asn Gly Gly Ser Val Lys Leu Tyr Pro Thr Asp Gln
 450 455 460
 Ser Thr Phe Asp Leu Leu Lys Asp Leu Glu Phe Ser Ala Gly Ser Pro
 465 470 475 480
 Ala Ser Lys Asp Thr Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile
 485 490 495
 Asp Glu Asn Leu Leu Ser Pro Leu Ala Gly Glu Asp Asp Pro Phe Leu
 500 505 510
 Leu Glu Gly Asn Thr Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp
 515 520 525
 Thr Lys Pro Lys Ile Lys Asp Thr Gly Asp Thr Ile Leu Ser Ser Pro
 530 535 540
 Ser Ser Val Ala Leu Pro Gln Val Lys Thr Glu Lys Asp Asp Phe Ile
 545 550 555 560
 Glu Leu Cys Thr Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Pro Val
 565 570 575
 Tyr Cys Gln Ala Ser Phe Ser Gly Thr Asn Ile Ile Gly Asn Lys Met
 580 585 590
 Ser Ala Ile Ser Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr
 595 600 605
 His Tyr Asp Met Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys
 610 615 620
 Pro Val Phe Asn Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp
 625 630 635 640
 Asn Arg Cys Gln Gly Ser Gly Glu Asp Ser Leu Thr Ser Leu Gly Ala
 645 650 655

Leu Asn Phe Pro Gly Arg Ser Val Phe Ser Asn Gly Tyr Ser Ser Pro
 660 665 670

Gly Met Arg Pro Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Ala Ala
 675 680 685

Thr Gly Pro Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser
 690 695 700

Gly Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe
 705 710 715 720

Lys Arg Ala Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn
 725 730 735

Asp Cys Ile Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg
 740 745 750

Tyr Arg Lys Cys Leu Gln Ala Gly Met Ala Asn Leu Glu Ala Arg Lys
 755 760 765

Thr Lys Lys Lys Ile Lys Gly Ile Gln Gln Ala Thr Ala Gly Val Ser
 770 775 780

Gln Asp Thr Ser Glu Asn Pro Asn Lys Thr Ile Val Pro Ala Ala Leu
 785 790 795 800

Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro
 805 810 815

Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Ala Trp
 820 825 830

Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala
 835 840 845

Ala Val Lys Trp Ala Lys Ala Ile Leu Gly Leu Arg Asn Leu His Leu
 850 855 860

Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala
 865 870 875 880

Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser Ser Gly Asn Leu Leu
 885 890 895

Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Ser Leu Pro
 900 905 910

Cys Met Tyr Asp Gln Cys Lys His Met Leu Phe Val Ser Ser Glu Leu
 915 920 925

Gln Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu
 930 935 940

Leu Leu Leu Ser Ser Val Pro Lys Glu Gly Leu Lys Ser Gln Glu Leu
 945 950 955 960

Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile
 965 970 975

Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln
 980 985 990

Leu Thr Lys Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu
 995 1000 1005

Thr Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu
 1010 1015 1020

Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys
 1025 1030 1035

Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln Lys
 1040 1045 1050

<210> 68
 <211> 158
 <212> PRT
 <213> Saccharomyces cerevisia

<400> 68

Met Ser Thr Val Pro Leu Val Tyr Ser Pro Val Asp Arg Glu Pro Leu
 1 5 10 15

His Asp Asn Ser Ala Asn Ile Lys Arg Pro Leu Gly Ser Phe Val Thr
 20 25 30

Ser Ser Ala Ala Cys Phe Lys Pro Leu Thr Ile Pro Gly Pro Thr Thr
 35 40 45

Pro Cys Ala Phe Val Met Ser Ala His Ser Ala Ile Leu Tyr Thr Pro
 50 55 60

Ala Glu Tyr Cys Asn Leu Thr Val Leu Pro Met Ser Ala Asn Phe Leu
 65 70 75 80

Ser Ser Lys Ser Lys Lys Leu Tyr Leu Ala Asp Asn Ala Phe Ser Gly
85 90 95

Leu Thr Val Pro Ser Met Glu Lys Ser Val Lys Ile Ser Thr Cys Val
100 105 110

Phe Ser Lys Gln Ile Leu Gly Pro Asn Ala Ser Thr Asn Ser Ser Asn
115 120 125

Ser Leu Val Val Arg Thr Ser Asn Glu Ala His Lys Phe Val Cys Phe
130 135 140

Ser Cys Met Ile Leu Asn Ser Leu Ala Ala Thr Gly Leu Gly
145 150 155

<210> 69
<211> 267
<212> PRT
<213> Saccharomyces cerevisia

<400> 69

Met Ser Lys Ala Thr Tyr Lys Glu Arg Ala Ala Thr His Pro Ser Pro
1 5 10 15

Val Ala Ala Lys Leu Phe Asn Ile Met His Glu Lys Gln Thr Asn Leu
20 25 30

Cys Ala Ser Leu Asp Val Arg Thr Thr Lys Glu Leu Leu Glu Leu Val
35 40 45

Glu Ala Leu Gly Pro Lys Ile Cys Leu Leu Lys Thr His Val Asp Ile
50 55 60

Leu Thr Asp Phe Ser Met Glu Gly Thr Val Lys Pro Leu Lys Ala Leu
65 70 75 80

Ser Ala Lys Tyr Asn Phe Leu Leu Phe Glu Asp Arg Lys Phe Ala Asp
85 90 95

Ile Gly Asn Thr Val Lys Leu Gln Tyr Ser Ala Gly Val Tyr Arg Ile
100 105 110

Ala Glu Trp Ala Asp Ile Thr Asn Ala His Gly Val Val Gly Pro Gly
115 120 125

Ile Val Ser Gly Leu Lys Gln Ala Ala Glu Glu Val Thr Lys Glu Pro
130 135 140

Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Cys Lys Gly Ser Leu Ser
145 150 155 160

Thr Gly Glu Tyr Thr Lys Gly Thr Val Asp Ile Ala Lys Ser Asp Lys
165 170 175

Asp Phe Val Ile Gly Phe Ile Ala Gln Arg Asp Met Gly Gly Arg Asp
180 185 190

Glu Gly Tyr Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp Asp
195 200 205

Lys Gly Asp Ala Leu Gly Gln Gln Tyr Arg Thr Val Asp Asp Val Val
210 215 220

Ser Thr Gly Ser Asp Ile Ile Ile Val Gly Arg Gly Leu Phe Ala Lys
225 230 235 240

Gly Arg Asp Ala Lys Val Glu Gly Glu Arg Tyr Arg Lys Ala Gly Trp
245 250 255

Glu Ala Tyr Leu Arg Arg Cys Gly Gln Gln Asn
260 265

<210> 70
<211> 286
<212> PRT
<213> Saccharomyces cerevisia

<400> 70

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1 5 10 15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
65 70 75 80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
85 90 95

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175

Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
 275 280 285